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(54) Title: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION OF VIRUS-LIKE PARTICLES (57) Abstract <p>The present invention relates to the efficient expression of HIV polypeptides in a variety of cell types, including, but not limited to, mammalian, insect, and plant cells. Synthetic expression cassettes encoding the HIV Gag-containing polypeptides are described, as are uses of the expression cassettes in applications including DNA immunization, generation of packaging cell lines, and production of Env-, tat- or Gag-containing proteins. The invention provides methods of producing Virus-Like Particles (VLPs), as well as, uses of the VLPs including, but not limited to, vehicles for the presentation of antigens and stimulation of immune response in subjects to whom the VLPs are administered.</p>		

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IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND
PRODUCTION OF VIRUS-LIKE PARTICLES

5 **TECHNICAL FIELD**

Synthetic expression cassettes encoding the HIV polypeptides (e.g., Gag-, pol-, prot-, reverse transcriptase, Env- or tat-containing polypeptides) are described, as are uses of the expression cassettes. The present invention relates to the efficient expression of HIV polypeptides in a variety of cell types. Further, the invention provides methods of producing Virus-Like Particles (VLPs), as well as, uses of the VLPs and high level expression of oligomeric envelope proteins.

15

BACKGROUND OF THE INVENTION

Acquired immune deficiency syndrome (AIDS) is recognized as one of the greatest health threats facing modern medicine. There is, as yet, no cure for this disease.

20

In 1983-1984, three groups independently identified the suspected etiological agent of AIDS. See, e.g., Barre-Sinoussi et al. (1983) Science 220:868-871; Montagnier et al., in Human T-Cell Leukemia Viruses (Gallo, Essex & Gross, eds., 1984); Vilmer et al. (1984) The Lancet 1:753; Popovic et al. (1984) Science 224:497-500; Levy et al. (1984) Science 225:840-842. These isolates were variously called lymphadenopathy-associated virus (LAV), human T-cell lymphotropic virus

type III (HTLV-III), or AIDS-associated retrovirus (ARV). All of these isolates are strains of the same virus, and were later collectively named Human Immunodeficiency Virus (HIV). With the isolation of a related

5 AIDS-causing virus, the strains originally called HIV are now termed HIV-1 and the related virus is called HIV-2. See, e.g., Guyader et al. (1987) *Nature* 326:662-669; Brun-Vezinet et al. (1986) *Science* 233:343-346; Clavel et al. (1986) *Nature* 324:691-695.

10 A great deal of information has been gathered about the HIV virus, however, to date an effective vaccine has not been identified. Several targets for vaccine development have been examined including the *env*, *Gag*, *pol* and *tat* gene products encoded by HIV.

15 Haas, et al., (*Current Biology* 6(3):315-324, 1996) suggested that selective codon usage by HIV-1 appeared to account for a substantial fraction of the inefficiency of viral protein synthesis. Andre, et al., (*J. Virol.* 72(2):1497-1503, 1998) described an increased immune
20 response elicited by DNA vaccination employing a synthetic gp120 sequence with optimized codon usage. Schneider, et al., (*J Virol.* 71(7):4892-4903, 1997) discuss inactivation of inhibitory (or instability) elements (INS) located within the coding sequences of the
25 *Gag* and *Gag*-protease coding sequences.

The *Gag* proteins of HIV-1 are necessary for the assembly of virus-like particles. HIV-1 *Gag* proteins are involved in many stages of the life cycle of the virus including, assembly, virion maturation after particle
30 release, and early post-entry steps in virus replication. The roles of HIV-1 *Gag* proteins are numerous and complex (Freed, E.O., *Virology* 251:1-15, 1998).

Wolf, et al., (PCT International Application, WO 96/30523, published 3 October 1996; European Patent Application, Publication No. 0 449 116 A1, published 2 October 1991) have described the use of altered pr55 Gag of HIV-1 to act as a non-infectious retroviral-like particulate carrier, in particular, for the presentation of immunologically important epitopes. Wang, et al., (Virology 200:524-534, 1994) describe a system to study assembly of HIV Gag- β -galactosidase fusion proteins into virions. They describe the construction of sequences encoding HIV Gag- β -galactosidase fusion proteins, the expression of such sequences in the presence of HIV Gag proteins, and assembly of these proteins into virus particles.

Recently, Shiver, et al., (PCT International Application, WO 98/34640, published 13 August 1998) described altering HIV-1 (CAM1) Gag coding sequences to produce synthetic DNA molecules encoding HIV Gag and modifications of HIV Gag. The codons of the synthetic molecules were codons preferred by a projected host cell.

The envelope protein of HIV-1 is a glycoprotein of about 160 kD (gp160). During virus infection of the host cell, gp160 is cleaved by host cell proteases to form gp120 and the integral membrane protein, gp41. The gp41 portion is anchored in (and spans) the membrane bilayer of virion, while the gp120 segment protrudes into the surrounding environment. As there is no covalent attachment between gp120 and gp41, free gp120 is released from the surface of virions and infected cells.

Haas, et al., (Current Biology 6(3):315-324, 1996) suggested that selective codon usage by HIV-1 appeared to account for a substantial fraction of the inefficiency of viral protein synthesis. Andre, et al., (J. Virol.

72(2):1497-1503, 1998) described an increased immune response elicited by DNA vaccination employing a synthetic gp120 sequence with optimized codon usage.

5 **SUMMARY OF THE INVENTION**

The present invention relates to improved expression of HIV *Env*-, *tat*-, *pol*-, *prot*-, reverse transcriptase, or *Gag*-containing polypeptides and production of virus-like particles.

10 In one embodiment the present invention includes an expression cassette, comprising a polynucleotide encoding an HIV *Gag* polypeptide comprising a sequence having at least 90% sequence identity to the sequence presented as SEQ ID NO:20. In certain embodiments, the polynucleotide
15 sequence encoding said *Gag* polypeptide comprises a sequence having at least 90% sequence identity to the sequence presented as SEQ ID NO:9 or SEQ ID NO:4. The expression cassettes may further include a polynucleotide sequence encoding an HIV *protease* polypeptide, for
20 example a nucleotide sequence having at least 90% sequence identity to a sequence selected from the group consisting of: SEQ ID NO:5, SEQ ID NO:78, and SEQ ID NO:79. The expression cassettes may further include a polynucleotide sequence encoding an HIV *reverse*
25 *transcriptase* polypeptide, for example a sequence having at least 90% sequence identity to a sequence selected from the group consisting of: SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, and SEQ ID NO:84. The expression cassettes may further include a polynucleotide
30 sequence encoding an HIV *tat* polypeptide, for example a sequence selected from the group consisting of: SEQ ID NO:87, SEQ ID NO:88, and SEQ ID NO:89. The expression cassettes may further include a polynucleotide sequence encoding an HIV *polymerase* polypeptide, for example a

sequence having at least 90% sequence identity to the sequence presented as SEQ ID NO:6. The expression cassettes may include a polynucleotide sequence encoding an HIV *polymerase* polypeptide, wherein (i) the nucleotide
5 sequence encoding said polypeptide comprises a sequence having at least 90% sequence identity to the sequence presented as SEQ ID NO:4, and (ii) wherein the sequence is modified by deletions of coding regions corresponding to reverse transcriptase and integrase. The expression
10 cassettes described above may preserves T-helper cell and CTL epitopes. The expression cassettes may further include a polynucleotide sequence encoding an HCV *core* polypeptide, for example a sequence having at least 90% sequence identity to the sequence presented as SEQ ID
15 NO:7.

In another aspect, the invention includes an expression cassette, comprising a polynucleotide sequence encoding a polypeptide including an HIV *Env* polypeptide, wherein the polynucleotide sequence encoding said *Env*
20 polypeptide comprises a sequence having at least 90% sequence identity to SEQ ID NO:71 (Figure 58) or SEQ ID NO:72 (Figure 59). In certain embodiments, the *Env* expression cassettes includes sequences flanking a V1 region but have a deletion in the V1 region itself, for
25 example the sequence presented as SEQ ID NO:65 (Figure 52, gp160.modUS4.delV1). In certain embodiments, the *Env* expression cassettes, include sequences flanking a V2 region but have a deletion in the V2 region itself, for example the sequences shown in SEQ ID NO:60 (Figure 47);
30 SEQ ID NO:66 (Figure 53); SEQ ID NO:34 (Figure 20); SEQ ID NO:37 (Figure 24); SEQ ID NO:40 (Figure 27); SEQ ID NO:43 (Figure 30); SEQ ID NO:46 (Figure 33); SEQ ID NO:76 (Figure 64) and SEQ ID NO:49 (Figure 36). In certain

embodiments, the Env expression cassettes include sequences flanking a V1/V2 region but have a deletion in the V1/V2 region itself, for example, SEQ ID NO:59 (Figure 46); SEQ ID NO:61 (Figure 48); SEQ ID NO:67 (Figure 54); SEQ ID NO:75 (Figure 63); SEQ ID NO:35 (Figure 21); SEQ ID NO:38 (Figure 25); SEQ ID NO:41 (Figure 28); SEQ ID NO:44 (Figure 31); SEQ ID NO:47 (Figure 34) and SEQ ID NO:50 (Figure 37). The Env-encoding expression cassettes may also include a mutated cleavage site that prevents the cleavage of a gp140 polypeptide into a gp120 polypeptide and a gp41 polypeptide, for example, SEQ ID NO:57 (Figure 44); SEQ ID NO:61 (Figure 48); SEQ ID NO:63 (Figure 50); SEQ ID NO:39 (Figure 26); SEQ ID NO:40 (Figure 27); SEQ ID NO:41 (Figure 28); SEQ ID NO:42 (Figure 29); SEQ ID NO:43 (Figure 30); SEQ ID NO:44 (Figure 31); SEQ ID NO:45 (Figure 32); SEQ ID NO:46 (Figure 33); and SEQ ID NO:47 (Figure 34). The Env expression cassettes may include a gp160 Env polypeptide or a polypeptide derived from a gp160 Env polypeptide, for example SEQ ID NO:64 (Figure 51); SEQ ID NO:65 (Figure 52); SEQ ID NO:66 (Figure 53); SEQ ID NO:67 (Figure 54); SEQ ID NO:68 (Figure 55); SEQ ID NO:75 (Figure 63); SEQ ID NO:73 (Figure 61); SEQ ID NO:48 (Figure 35); SEQ ID NO:49 (Figure 36); SEQ ID NO:50 (Figure 37); SEQ ID NO:76 (Figure 64); and SEQ ID NO:74 (Figure 62). The Env expression cassettes may include a gp140 Env polypeptide or a polypeptide derived from a gp140 Env polypeptide, for example SEQ ID NO:56 (Figure 43); SEQ ID NO:57 (Figure 44); SEQ ID NO:58 (Figure 45); SEQ ID NO:59 (Figure 46); SEQ ID NO:60 (Figure 47); SEQ ID NO:61 (Figure 48); SEQ ID NO:62 (Figure 49); SEQ ID NO:63 (Figure 50); SEQ ID NO:36 (Figure 23); SEQ ID NO:37 (Figure 24); SEQ ID NO:38 (Figure 25); SEQ ID NO:39

(Figure 26); SEQ ID NO:40 (Figure 27); SEQ ID NO:41 (Figure 28); SEQ ID NO:42 (Figure 29); SEQ ID NO:43 (Figure 30); SEQ ID NO:44 (Figure 31); SEQ ID NO:45 (Figure 32); SEQ ID NO:46 (Figure 33); and SEQ ID NO:47 (Figure 34). The Env expression cassettes may also include a gp120 Env polypeptide or a polypeptide derived from a gp120 Env polypeptide, for example SEQ ID NO:54 (Figure 41); and SEQ ID NO:55 (Figure 42); SEQ ID NO:33 (Figure 19); SEQ ID NO:34 (Figure 20); and SEQ ID NO:35 (Figure 21). The Env expression cassettes may include an Env polypeptide lacking the amino acids corresponding to residues 128 to about 194, relative to strains SF162 or US4, for example, SEQ ID NO:55 (Figure 42); SEQ ID NO:62 (Figure 49); SEQ ID NO:63 (Figure 50); and SEQ ID NO:68 (Figure 55).

In another aspect, the invention includes a recombinant expression system for use in a selected host cell, comprising, one or more of the expression cassettes described herein operably linked to control elements compatible with expression in the selected host cell. The expression cassettes may be included on one or on multiple vectors and may use the same or different promoters. Exemplary control elements include a transcription promoter (e.g., CMV, CMV+intron A, SV40, RSV, HIV-Ltr, MMLV-ltr, and metallothionein), a transcription enhancer element, a transcription termination signal, polyadenylation sequences, sequences for optimization of initiation of translation, and translation termination sequences.

In another aspect, the invention includes a recombinant expression system for use in a selected host cell, comprising, any one of the expression cassettes described herein operably linked to control elements

compatible with expression in the selected host cell. Exemplary control elements include, but are not limited to, a transcription promoter (e.g., CMV, CMV+intron A, SV40, RSV, HIV-LTR, MMLV-LTR, and metallothionein), a
5 transcription enhancer element, a transcription termination signal, polyadenylation sequences, sequences for optimization of initiation of translation, and translation termination sequences.

In yet another aspect, the invention includes a cell
10 comprising one or more of the expression cassettes described herein operably linked to control elements compatible with expression in the cell. The cell can be, for example, a mammalian cell (e.g., BHK, VERO, HT1080, 293, RD, COS-7, or CHO cells), an insect cell (e.g.,
15 *Trichoplusia ni* (Tn5) or Sf9), a bacterial cell, a plant cell, a yeast cell, an antigen presenting cell (e.g., primary, immortalized or tumor-derived lymphoid cells such as macrophages, monocytes, dendritic cells, B-cells, T-cells, stem cells, and progenitor cells thereof).

20 In another aspect, the invention includes methods for producing a polypeptide including HIV *Gag*-, *prot*-, *pol*-, *reverse transcriptase*, *Env*- or *Tat*-containing polypeptide sequences, said method comprising, incubating the cells comprising one or more the expression cassettes
25 describe herein, under conditions for producing said polypeptide.

In yet another aspect, the invention includes compositions for generating an immunological response, comprising one or more of the expression cassettes
30 described herein. In certain embodiments, the compositions also include an adjuvant.

In a still further aspect, the invention includes methods of generating an immune response in a subject, comprising introducing a composition comprising one or

more of the expression cassettes described herein into the subject under conditions that are compatible with expression of said expression cassette in the subject. In certain embodiments, the expression cassette is
5 introduced using a gene delivery vector. More than one expression cassette may be introduced using one or more gene delivery vectors.

In yet another aspect, the invention includes a purified polynucleotide comprising a polynucleotide
10 sequence encoding a polypeptide including an HIV Env polypeptide, wherein the polynucleotide sequence encoding said Env polypeptide comprises a sequence having at least 90% sequence identity to SEQ ID NO:71 (Figure 58) or SEQ ID NO:72 (Figure 59). Further exemplary purified
15 polynucleotide sequences were presented above.

The polynucleotides of the present invention can be produced by recombinant techniques, synthetic techniques, or combinations thereof.

In another embodiment, the invention includes a
20 method for producing a polypeptide including HIV Gag polypeptide sequences, where the method comprises incubating any of the above cells containing an expression cassette of interest under conditions for producing the polypeptide.

25 The invention further includes, a method for producing virus-like particles (VLPs) where the method comprises incubating any of the above-described cells containing an expression cassette of interest under conditions for producing VLPs.

30 In another aspect the invention includes a method for producing a composition of virus-like particles (VLPs) where, any of the above-described cells containing an expression cassette of interest are incubated under

conditions for producing VLPs, and the VLPs are substantially purified to produce a composition of VLPs.

In a further embodiment of the present invention, packaging cell lines are produced using the expression
5 cassettes of the present invention. For example, a cell line useful for packaging lentivirus vectors comprises suitable host cells that have an expression vector containing an expression cassette of the present invention wherein said polynucleotide sequence is
10 operably linked to control elements compatible with expression in the host cell. In a preferred embodiment, such host cells may be transfected with one or more expression cassettes having a polynucleotide sequence that encodes an HIV *polymerase* polypeptide or
15 polypeptides derived therefrom, for example, where the nucleotide sequence encoding said polypeptide comprises a sequence having at least 90% sequence identity to the sequence presented as SEQ ID NO:6. Further, the HIV *polymerase* polypeptide may be modified by deletions of
20 coding regions corresponding to reverse transcriptase and integrase. Such a polynucleotide sequence may preserve T-helper cell and CTL epitopes, for example when used in a vaccine application. In addition, the polynucleotide sequence may also include other polypeptides. Further,
25 polynucleotide sequences encoding additional polypeptides whose expression are useful for packaging cell line function may also be utilized.

In another aspect, the present invention includes a gene delivery or vaccine vector for use in a subject,
30 where the vector is a suitable gene delivery vector for use in the subject, and the vector comprises one or more of any of the expression cassettes of the present

invention where the polynucleotide sequences of interest are operably linked to control elements compatible with expression in the subject. Such gene delivery vectors can be used in a method of DNA immunization of a subject, 5 for example, by introducing a gene delivery vector into the subject under conditions that are compatible with expression of the expression cassette in the subject. Gene delivery vectors useful in the practice of the present invention include, but are not limited to, 10 nonviral vectors, bacterial plasmid vectors, viral vectors, particulate carriers (where the vector is coated on a polylactide co-glycolide particles, gold or tungsten particle, for example, the coated particle can be delivered to a subject cell using a gene gun), liposome 15 preparations, and viral vectors (e.g., vectors derived from alphaviruses, pox viruses, and vaccinia viruses, as well as, retroviral vectors, including, but not limited to, lentiviral vectors). Alphavirus-derived vectors include, for example, an alphavirus cDNA construct, a 20 recombinant alphavirus particle preparation and a eukaryotic layered vector initiation system. In one embodiment, the subject is a vertebrate, preferably a mammal, and in a further embodiment the subject is a human.

25 The invention further includes a method of generating an immune response in a subject, where cells of a subject are transfected with any of the above-described gene delivery vectors (e.g., alphavirus constructs; alphavirus cDNA constructs; eukaryotic 30 layered vector initiation systems (see, e.g., U.S. Patent Number 5,814,482 for description of suitable eukaryotic layered vector initiation systems); alphavirus particle

preparations; etc.) under conditions that permit the expression of a selected polynucleotide and production of a polypeptide of interest (i.e., encoded by any expression cassette of the present invention), thereby
5 eliciting an immunological response to the polypeptide. Transfection of the cells may be performed *ex vivo* and the transfected cells are reintroduced into the subject. Alternately, or in addition, the cells may be transfected *in vivo* in the subject. The immune response may be
10 humoral and/or cell-mediated (cellular).

Further embodiments of the present invention include purified polynucleotides. In one embodiment, the purified polynucleotide comprises a polynucleotide sequence having at least 90% sequence identity to the
15 sequence presented as SEQ ID NO:20, and complements thereof. In another embodiment, the purified polynucleotide comprises a polynucleotide sequence encoding an HIV Gag polypeptide, wherein the polynucleotide sequence comprises a sequence having at
20 least 90% sequence identity to the sequence presented as SEQ ID NO:20, and complements thereof. In still another embodiment, the purified polynucleotide comprises a polynucleotide sequence encoding an HIV Gag polypeptide, wherein the polynucleotide sequence comprises a sequence
25 having at least 90% sequence identity to the sequence presented as SEQ ID NO:9, and complements thereof. In further embodiments the polynucleotide sequence comprises a sequence having at least 90% sequence identity to one of the following sequences: SEQ ID NO:4, SEQ ID NO:5, SEQ
30 ID NO:6, SEQ ID NO:7, and complements thereof.

The polynucleotides of the present invention can be produced by recombinant techniques, synthetic techniques, or combinations thereof.

These and other embodiments of the present invention will readily occur to those of ordinary skill in the art in view of the disclosure herein.

5 **BRIEF DESCRIPTION OF THE FIGURES**

Figure 1 shows the locations of the inactivation sites for the native HIV-1SF2 Gag protein coding sequence.

10 Figure 2 shows the locations of the inactivation sites for the native HIV-1SF2 Gag-protease protein coding sequence.

Figures 3A and 3B show electron micrographs of virus-like particles. Figure 3A shows immature p55Gag virus-like particles in COS-7 cells transfected with a
15 synthetic HIV-1_{SF2} gag construct while Figure 3B shows mature (arrows) and immature VLP in cells transfected with a modified HIV-1_{SF2} gagprotease construct (GP2, SEQ ID NO:70). Transfected cells were fixed at 24 h (gag) or 48 h (gagprotease) post-transfection and subsequently
20 analyzed by electron microscopy (magnification at 100,000X). Cells transfected with vector alone (pCMVKm2) served as negative control (data not shown).

Figure 4 presents an image of samples from a series of fractions which were electrophoresed on an 8-16% SDS
25 polyacrylamide gel and the resulting bands visualized by commassie blue staining. The results show that the native p55 Gag virus-like particles (VLPs) banded at a sucrose density of range of 1.15 - 1.19 g/ml with the peak at approximately 1.17 g/ml.

30 Figure 5 presents an image similar to Figure 4 where the analysis was performed using Gag VLPs produced by a synthetic Gag expression cassette.

Figure 6 presents a comparison of the total amount of purified HIV p55 Gag from several preparations obtained from two baculovirus expression cassettes encoding native and modified Gag.

5 Figure 7 presents an alignment of modified coding sequences of the present invention including a synthetic Gag expression cassette (SEQ ID NO:4), a synthetic Gag-protease expression cassette (SEQ ID NO:5), and a synthetic Gag-polymerase expression cassette (SEQ ID
10 NO:6). A common region (Gag-common; SEQ ID NO:9) extends from position 1 to position 1262.

Figure 8 presents an image of wild-type Gag-HCV core expression samples from a series of fractions which were electrophoresed on an 8-16% SDS polyacrylamide gel and
15 the resulting bands visualized by commassie staining.

Figure 9 shows the results of Western blot analysis of the gel shown presented in Figure 8.

Figure 10 presents results similar to those shown in Figure 9. The results in Figure 10 indicate that the
20 main HCV Core-specific reactivity migrates at an approximate molecular weight of 72,000 kD, which is in accordance with the predicted molecular weight of the Gag-HCV core chimeric protein.

Figures 11A to 11D present a comparison of AT
25 content, in percent, of cDNAs corresponding to an unstable human mRNA (human IFN γ mRNA; 11A), wild-type HIV Gag native RNA (11B), a stable human mRNA (human GAPDH mRNA; 11C), and synthetic HIV Gag RNA (11D).

Figure 12 shows the location of the inactivation
30 sites for the native HIV-1SF2 Gag-polymerase sequence.

Figure 13A presents a vector map of pESN2dhfr.

Figure 13B presents a map of the pCMVIII vector.

Figure 14 presents a vector map of pCMV-LINK.

Figure 15 presents a schematic diagram showing the relationships between the following forms of the HIV Env polypeptide: gp160, gp140, gp120, and gp41.

Figure 16 depicts the nucleotide sequence of wild-type gp120 from SF162 (SEQ ID NO:30).

Figure 17 depicts the nucleotide sequence of the wild-type gp140 from SF162 (SEQ ID NO:31).

Figure 18 depicts the nucleotide sequence of the wild-type gp160 from SF162 (SEQ ID NO:32).

Figure 19 depicts the nucleotide sequence of the construct designated gp120.modSF162 (SEQ ID NO:33).

Figure 20 depicts the nucleotide sequence of the construct designated gp120.modSF162.delV2 (SEQ ID NO:34).

Figure 21 depicts the nucleotide sequence of the construct designated gp120.modSF162.delV1/V2 (SEQ ID NO:35).

Figures 22A-H show the percent A-T content over the length of the sequences for IFN γ (Figures 2C and 2G); native gp160 Env US4 and SF162 (Figures 2A and 2E, respectively); GAPDH (Figures 2D and 2H); and the synthetic gp160 Env for US4 and SF162 (Figures 2B and 2F, respectively).

Figure 23 depicts the nucleotide sequence of the construct designated gp140.modSF162 (SEQ ID NO:36).

Figure 24 depicts the nucleotide sequence of the construct designated gp140.modSF162.delV2 (SEQ ID NO:37).

Figure 25 depicts the nucleotide sequence of the construct designated gp140.modSF162.delV1/V2 (SEQ ID NO:38).

Figure 26 depicts the nucleotide sequence of the construct designated gp140.mut.modSF162 (SEQ ID NO:39).

Figure 27 depicts the nucleotide sequence of the construct designated gp140.mut.modSF162.delV2 (SEQ ID NO:40).

Figure 28 depicts the nucleotide sequence of the construct designated gp140.mut.modSF162.delV1/V2 (SEQ ID NO:41).

5 Figure 29 depicts the nucleotide sequence of the construct designated gp140.mut7.modSF162 (SEQ ID NO:42).

Figure 30 depicts the nucleotide sequence of the construct designated gp140.mut7.modSF162.delV2 (SEQ ID NO:43).

10 Figure 31 depicts the nucleotide sequence of the construct designated gp140.mut7.modSF162.delV1/V2 (SEQ ID NO:44).

Figure 32 depicts the nucleotide sequence of the construct designated gp140.mut8.modSF162 (SEQ ID NO:45).

15 Figure 33 depicts the nucleotide sequence of the construct designated gp140.mut8.modSF162.delV2 (SEQ ID NO:46).

Figure 34 depicts the nucleotide sequence of the construct designated gp140.mut8.modSF162.delV1/V2 (SEQ ID NO:47).

20 Figure 35 depicts the nucleotide sequence of the construct designated gp160.modSF162 (SEQ ID NO:48).

Figure 36 depicts the nucleotide sequence of the construct designated gp160.modSF162.delV2 (SEQ ID NO:49).

25 Figure 37 depicts the nucleotide sequence of the construct designated gp160.modSF162.delV1/V2 (SEQ ID NO:50).

Figure 38 depicts the nucleotide sequence of the wild-type gp120 from US4 (SEQ ID NO:51).

30 Figure 39 depicts the nucleotide sequence of the wild-type gp140 from US4 (SEQ ID NO:52).

Figure 40 depicts the nucleotide sequence of the wild-type gp160 from US4 (SEQ ID NO:53).

Figure 41 depicts the nucleotide sequence of the construct designated gp120.modUS4 (SEQ ID NO:54).

Figure 42 depicts the nucleotide sequence of the construct designated gp120.modUS4.del 128-194 (SEQ ID NO:55).

5 Figure 43 depicts the nucleotide sequence of the construct designated gp140.modUS4 (SEQ ID NO:56).

Figure 44 depicts the nucleotide sequence of the construct designated gp140.mut.modUS4 (SEQ ID NO:57).

Figure 45 depicts the nucleotide sequence of the construct designated gp140.TM.modUS4 (SEQ ID NO:58).

10 Figure 46 depicts the nucleotide sequence of the construct designated gp140.modUS4.delV1/V2 (SEQ ID NO:59).

Figure 47 depicts the nucleotide sequence of the construct designated gp140.modUS4.delV2 (SEQ ID NO:60).

15 Figure 48 depicts the nucleotide sequence of the construct designated gp140.mut.modUS4.delV1/V2 (SEQ ID NO:61).

20 Figure 49 depicts the nucleotide sequence of the construct designated gp140.modUS4.del 128-194 (SEQ ID NO:62).

Figure 50 depicts the nucleotide sequence of the construct designated gp140.mut.modUS4.del 128-194 (SEQ ID NO:63).

25 Figure 51 depicts the nucleotide sequence of the construct designated gp160.modUS4 (SEQ ID NO:64).

Figure 52 depicts the nucleotide sequence of the construct designated gp160.modUS4.delV1 (SEQ ID NO:65).

Figure 53 depicts the nucleotide sequence of the construct designated gp160.modUS4.delV2 (SEQ ID NO:66).

30 Figure 54 depicts the nucleotide sequence of the construct designated gp160.modUS4.delV1/V2 (SEQ ID NO:67).

Figure 55 depicts the nucleotide sequence of the construct designated gp160.modUS4.del 128-194 (SEQ ID NO:68).

5 Figure 56 depicts the nucleotide sequence of the common region of Env from wild-type US4 (SEQ ID NO:69).

Figure 57 depicts the nucleotide sequence of the common region of Env from wild-type SF162 (SEQ ID NO:70).

10 Figure 58 depicts the nucleotide sequence of synthetic sequences corresponding to the common region of Env from US4 (SEQ ID NO:71).

Figure 59 depicts the nucleotide sequence of synthetic sequences corresponding to the common region of Env from SF162 (SEQ ID NO:72).

15 Figure 60 presents a schematic representation of an Env polypeptide purification strategy.

Figure 61 depicts the nucleotide sequence of the bicistronic construct designated gp160.modUS4.Gag.modSF2 (SEQ ID NO:73).

20 Figure 62 depicts the nucleotide sequence of the bicistronic construct designated gp160.modSF162.Gag.modSF2 (SEQ ID NO:74).

Figure 63 depicts the nucleotide sequence of the bicistronic construct designated gp160.modUS4.-delV1/V2.Gag.modSF2 (SEQ ID NO:75).

25 Figure 64 depicts the nucleotide sequence of the bicistronic construct designated gp160.modSF162.delV2.Gag.modSF2 (SEQ ID NO:76).

30 Figures 65A-65F show micrographs of 293T cells transfected with the following polypeptide encoding sequences: Figure 65A, gag.modSF2; Figure 65B, gp160.modUS4; Figure 65C, gp160.modUS4.delV1/V2.gag.modSF2 (bicistronic Env and Gag); Figures 65D and 65E, gp160.modUS4.delV1/V2 and

gag.modSF2; and Figure 65F, gp120.modSF162.delV2 and gag.modSF2.

Figures 66A and 66B present alignments of selected modified coding sequences of the present invention including a common region defined for each group of synthetic *Env* expression cassettes. Figure 66A presents alignments of modified SF162 sequences. Figure 66B presents alignments of modified US4 sequences. The SEQ ID NOs for these sequences are presented in Tables 1A and 1B.

Figure 67 shows the ELISA titers (binding antibodies) obtained in two rhesus macaques (H445, lines with solid black dots; and J408, lines with open squares). The y-axis is the end-point gp140 ELISA titers and the x-axis shows weeks post-immunization. The dashed lines at 0, 4, and 8 weeks represent DNA immunizations. The alternating dash/dotted line at 27 weeks indicates a DNA plus protein boost immunization.

Figure 68 (SEQ ID NO:77) depicts the wild-type nucleotide sequence of Gag reverse transcriptase from SF2.

Figure 69 (SEQ ID NO:78) depicts the nucleotide sequence of the construct designated GP1.

Figure 70 (SEQ ID NO:79) depicts the nucleotide sequence of the construct designated GP2.

Figure 71 (SEQ ID NO:80) depicts the nucleotide sequence of the construct designated FS(+).protinact.RTopt.YM. FS(+) indicates that there is a frameshift in the GagPol coding sequence.

Figure 72 (SEQ ID NO:81) depicts the nucleotide sequence of the construct designated FS(+).protinact.RTopt.YMWM.

Figure 73 (SEQ ID NO:82) depicts the nucleotide sequence of the construct designated FS(-

).protmod.RTopt.YM. FS(-) indicates that there is no frameshift in the GagPol coding sequence.

Figure 74 (SEQ ID NO:83) depicts the nucleotide sequence of the construct designated

5 FS(-).protmod.RTopt.YMWM.

Figure 75 (SEQ ID NO:84) depicts the nucleotide sequence of the construct designated FS(-).protmod.RTopt(+).

10 Figure 76 (SEQ ID NO:85) depicts the nucleotide sequence of wild type Tat from isolate SF162.

Figure 77 (SEQ ID NO:86) depicts the amino acid sequence of the tat polypeptide.

15 Figure 78 (SEQ ID NO:87) depicts the nucleotide sequence of a synthetic Tat construct designated Tat.SF162.opt.

20 Figure 79 (SEQ ID NO:88) depicts the nucleotide sequence of a synthetic Tat construct designated tat.cys22.sf162.opt. The construct encodes a tat polypeptide in which the cystein residue at position 22 of the wild type Tat polypeptide is replaced by a glycine residue.

Figures 80A to 80E are an alignment of the nucleotide sequences of the constructs designated Gag.mod.SF2, GP1 (SEQ ID NO:78), and GP2 (SEQ ID NO:79).

25 Figure 81 (SEQ ID NO:89) depicts the nucleotide sequence of the construct designated tataminoSF162.opt, which encodes the amino terminus of that tat protein. The codon encoding the cystein-22 residue is underlined.

30 Figure 82 (SEQ ID NO:90) depicts the amino acid sequence of the polypeptide encoded by the construct designated tat.cys22.SF162.opt (SEQ ID NO:88).

DETAILED DESCRIPTION OF THE INVENTION

The practice of the present invention will employ, unless otherwise indicated, conventional methods of chemistry, biochemistry, molecular biology, immunology and pharmacology, within the skill of the art. Such techniques are explained fully in the literature. See, e.g., *Remington's Pharmaceutical Sciences*, 18th Edition (Easton, Pennsylvania: Mack Publishing Company, 1990); *Methods In Enzymology* (S. Colowick and N. Kaplan, eds., Academic Press, Inc.); and *Handbook of Experimental Immunology*, Vols. I-IV (D.M. Weir and C.C. Blackwell, eds., 1986, Blackwell Scientific Publications); Sambrook, et al., *Molecular Cloning: A Laboratory Manual* (2nd Edition, 1989); *Short Protocols in Molecular Biology*, 4th ed. (Ausubel et al. eds., 1999, John Wiley & Sons); *Molecular Biology Techniques: An Intensive Laboratory Course*, (Ream et al., eds., 1998, Academic Press); *PCR (Introduction to Biotechniques Series)*, 2nd ed. (Newton & Graham eds., 1997, Springer Verlag).

As used in this specification and the appended claims, the singular forms "a," "an" and "the" include plural references unless the content clearly dictates otherwise. Thus, for example, reference to "an antigen" includes a mixture of two or more such agents.

1. DEFINITIONS

In describing the present invention, the following terms will be employed, and are intended to be defined as indicated below.

"Synthetic" sequences, as used herein, refers to Env-, tat- or Gag-encoding polynucleotides whose expression has been optimized as described herein, for example, by codon substitution, deletions, replacements and/or inactivation of inhibitory sequences. "Wild-type"

or "native" sequences, as used herein, refers to polypeptide encoding sequences that are essentially as they are found in nature, e.g., Gag encoding sequences as found in the isolate HIV-1SF2 or Env encoding sequences as found in the isolates HIV-1SF162 or HIV1US4.

As used herein, the term "virus-like particle" or "VLP" refers to a nonreplicating, viral shell, derived from any of several viruses discussed further below. VLPs are generally composed of one or more viral proteins, such as, but not limited to those proteins referred to as capsid, coat, shell, surface and/or envelope proteins, or particle-forming polypeptides derived from these proteins. VLPs can form spontaneously upon recombinant expression of the protein in an appropriate expression system. Methods for producing particular VLPs are known in the art and discussed more fully below. The presence of VLPs following recombinant expression of viral proteins can be detected using conventional techniques known in the art, such as by electron microscopy, biophysical characterization, and the like. See, e.g., Baker et al., *Biophys. J.* (1991) 60:1445-1456; Hagensee et al., *J. Virol.* (1994) 68:4503-4505. For example, VLPs can be isolated by density gradient centrifugation and/or identified by characteristic density banding (e.g., Example 7). Alternatively, cryoelectron microscopy can be performed on vitrified aqueous samples of the VLP preparation in question, and images recorded under appropriate exposure conditions.

By "particle-forming polypeptide" derived from a particular viral protein is meant a full-length or near full-length viral protein, as well as a fragment thereof, or a viral protein with internal deletions, which has the ability to form VLPs under conditions that favor VLP

formation. Accordingly, the polypeptide may comprise the full-length sequence, fragments, truncated and partial sequences, as well as analogs and precursor forms of the reference molecule. The term therefore intends

5 deletions, additions and substitutions to the sequence, so long as the polypeptide retains the ability to form a VLP. Thus, the term includes natural variations of the specified polypeptide since variations in coat proteins often occur between viral isolates. The term also

10 includes deletions, additions and substitutions that do not naturally occur in the reference protein, so long as the protein retains the ability to form a VLP. Preferred substitutions are those which are conservative in nature, i.e., those substitutions that take place within a family

15 of amino acids that are related in their side chains. Specifically, amino acids are generally divided into four families: (1) acidic -- aspartate and glutamate; (2) basic -- lysine, arginine, histidine; (3) non-polar -- alanine, valine, leucine, isoleucine, proline,

20 phenylalanine, methionine, tryptophan; and (4) uncharged polar -- glycine, asparagine, glutamine, cystine, serine, threonine, tyrosine. Phenylalanine, tryptophan, and tyrosine are sometimes classified as aromatic amino acids.

25 An "antigen" refers to a molecule containing one or more epitopes (either linear, conformational or both) that will stimulate a host's immune system to make a humoral and/or cellular antigen-specific response. The term is used interchangeably with the term "immunogen."

30 Normally, a B-cell epitope will include at least about 5 amino acids but can be as small as 3-4 amino acids. A T-cell epitope, such as a CTL epitope, will include at least about 7-9 amino acids, and a helper T-cell epitope at least about 12-20 amino acids. Normally, an epitope

will include between about 7 and 15 amino acids, such as, 9, 10, 12 or 15 amino acids. The term "antigen" denotes both subunit antigens, (i.e., antigens which are separate and discrete from a whole organism with which the antigen is associated in nature), as well as, killed, attenuated or inactivated bacteria, viruses, fungi, parasites or other microbes. Antibodies such as anti-idiotypic antibodies, or fragments thereof, and synthetic peptide mimotopes, which can mimic an antigen or antigenic determinant, are also captured under the definition of antigen as used herein. Similarly, an oligonucleotide or polynucleotide which expresses an antigen or antigenic determinant *in vivo*, such as in gene therapy and DNA immunization applications, is also included in the definition of antigen herein.

For purposes of the present invention, antigens can be derived from any of several known viruses, bacteria, parasites and fungi, as described more fully below. The term also intends any of the various tumor antigens. Furthermore, for purposes of the present invention, an "antigen" refers to a protein which includes modifications, such as deletions, additions and substitutions (generally conservative in nature), to the native sequence, so long as the protein maintains the ability to elicit an immunological response, as defined herein. These modifications may be deliberate, as through site-directed mutagenesis, or may be accidental, such as through mutations of hosts which produce the antigens.

An "immunological response" to an antigen or composition is the development in a subject of a humoral and/or a cellular immune response to an antigen present in the composition of interest. For purposes of the present invention, a "humoral immune response" refers to

an immune response mediated by antibody molecules, while a "cellular immune response" is one mediated by T-lymphocytes and/or other white blood cells. One important aspect of cellular immunity involves an antigen-specific response by cytolytic T-cells ("CTL"s). CTLs have specificity for peptide antigens that are presented in association with proteins encoded by the major histocompatibility complex (MHC) and expressed on the surfaces of cells. CTLs help induce and promote the destruction of intracellular microbes, or the lysis of cells infected with such microbes. Another aspect of cellular immunity involves an antigen-specific response by helper T-cells. Helper T-cells act to help stimulate the function, and focus the activity of, nonspecific effector cells against cells displaying peptide antigens in association with MHC molecules on their surface. A "cellular immune response" also refers to the production of cytokines, chemokines and other such molecules produced by activated T-cells and/or other white blood cells, including those derived from CD4+ and CD8+ T-cells.

A composition or vaccine that elicits a cellular immune response may serve to sensitize a vertebrate subject by the presentation of antigen in association with MHC molecules at the cell surface. The cell-mediated immune response is directed at, or near, cells presenting antigen at their surface. In addition, antigen-specific T-lymphocytes can be generated to allow for the future protection of an immunized host.

The ability of a particular antigen to stimulate a cell-mediated immunological response may be determined by a number of assays, such as by lymphoproliferation (lymphocyte activation) assays, CTL cytotoxic cell assays, or by assaying for T-lymphocytes specific for the

antigen in a sensitized subject. Such assays are well known in the art. See, e.g., Erickson et al., *J. Immunol.* (1993) 151:4189-4199; Doe et al., *Eur. J. Immunol.* (1994) 24:2369-2376. Recent methods of measuring cell-mediated immune response include measurement of intracellular cytokines or cytokine secretion by T-cell populations, or by measurement of epitope specific T-cells (e.g., by the tetramer technique) (reviewed by McMichael, A.J., and O'Callaghan, C.A., *J. Exp. Med.* 187(9)1367-1371, 1998; Mcheyzer-Williams, M.G., et al, *Immunol. Rev.* 150:5-21, 1996; Lalvani, A., et al, *J. Exp. Med.* 186:859-865, 1997).

Thus, an immunological response as used herein may be one which stimulates the production of CTLs, and/or the production or activation of helper T- cells. The antigen of interest may also elicit an antibody-mediated immune response. Hence, an immunological response may include one or more of the following effects: the production of antibodies by B-cells; and/or the activation of suppressor T-cells and/or $\gamma\delta$ T-cells directed specifically to an antigen or antigens present in the composition or vaccine of interest. These responses may serve to neutralize infectivity, and/or mediate antibody-complement, or antibody dependent cell cytotoxicity (ADCC) to provide protection to an immunized host. Such responses can be determined using standard immunoassays and neutralization assays, well known in the art.

An "immunogenic composition" is a composition that comprises an antigenic molecule where administration of the composition to a subject results in the development in the subject of a humoral and/or a cellular immune response to the antigenic molecule of interest.

By "subunit vaccine" is meant a vaccine composition which includes one or more selected antigens but not all antigens, derived from or homologous to, an antigen from a pathogen of interest such as from a virus, bacterium, parasite or fungus. Such a composition is substantially free of intact pathogen cells or pathogenic particles, or the lysate of such cells or particles. Thus, a "subunit vaccine" can be prepared from at least partially purified (preferably substantially purified) immunogenic polypeptides from the pathogen, or analogs thereof. The method of obtaining an antigen included in the subunit vaccine can thus include standard purification techniques, recombinant production, or synthetic production.

"Substantially purified" general refers to isolation of a substance (compound, polynucleotide, protein, polypeptide, polypeptide composition) such that the substance comprises the majority percent of the sample in which it resides. Typically in a sample a substantially purified component comprises 50%, preferably 80%-85%, more preferably 90-95% of the sample. Techniques for purifying polynucleotides and polypeptides of interest are well-known in the art and include, for example, ion-exchange chromatography, affinity chromatography and sedimentation according to density.

A "coding sequence" or a sequence which "encodes" a selected polypeptide, is a nucleic acid molecule which is transcribed (in the case of DNA) and translated (in the case of mRNA) into a polypeptide *in vivo* when placed under the control of appropriate regulatory sequences (or "control elements"). The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxy) terminus. A coding sequence can include, but

is not limited to, cDNA from viral, procaryotic or eucaryotic mRNA, genomic DNA sequences from viral or procaryotic DNA, and even synthetic DNA sequences. A transcription termination sequence may be located 3' to the coding sequence.

Typical "control elements", include, but are not limited to, transcription promoters, transcription enhancer elements, transcription termination signals, polyadenylation sequences (located 3' to the translation stop codon), sequences for optimization of initiation of translation (located 5' to the coding sequence), and translation termination sequences, see e.g., McCaughan et al. (1995) *PNAS USA* 92:5431-5435; Kochetov et al (1998) *FEBS Letts.* 440:351-355.

A "nucleic acid" molecule can include, but is not limited to, procaryotic sequences, eucaryotic mRNA, cDNA from eucaryotic mRNA, genomic DNA sequences from eucaryotic (e.g., mammalian) DNA, and even synthetic DNA sequences. The term also captures sequences that include any of the known base analogs of DNA and RNA.

"Operably linked" refers to an arrangement of elements wherein the components so described are configured so as to perform their usual function. Thus, a given promoter operably linked to a coding sequence is capable of effecting the expression of the coding sequence when the proper enzymes are present. The promoter need not be contiguous with the coding sequence, so long as it functions to direct the expression thereof. Thus, for example, intervening untranslated yet transcribed sequences can be present between the promoter sequence and the coding sequence and the promoter sequence can still be considered "operably linked" to the coding sequence.

"Recombinant" as used herein to describe a nucleic acid molecule means a polynucleotide of genomic, cDNA, semisynthetic, or synthetic origin which, by virtue of its origin or manipulation: (1) is not associated with
5 all or a portion of the polynucleotide with which it is associated in nature; and/or (2) is linked to a polynucleotide other than that to which it is linked in nature. The term "recombinant" as used with respect to a protein or polypeptide means a polypeptide produced by
10 expression of a recombinant polynucleotide. "Recombinant host cells," "host cells," "cells," "cell lines," "cell cultures," and other such terms denoting procaryotic microorganisms or eucaryotic cell lines cultured as unicellular entities, are used interchangeably, and refer
15 to cells which can be, or have been, used as recipients for recombinant vectors or other transfer DNA, and include the progeny of the original cell which has been transfected. It is understood that the progeny of a single parental cell may not necessarily be completely
20 identical in morphology or in genomic or total DNA complement to the original parent, due to accidental or deliberate mutation. Progeny of the parental cell which are sufficiently similar to the parent to be characterized by the relevant property, such as the
25 presence of a nucleotide sequence encoding a desired peptide, are included in the progeny intended by this definition, and are covered by the above terms.

Techniques for determining amino acid sequence "similarity" are well known in the art. In general,
30 "similarity" means the exact amino acid to amino acid comparison of two or more polypeptides at the appropriate place, where amino acids are identical or possess similar chemical and/or physical properties such as charge or hydrophobicity. A so-termed "percent similarity" then

can be determined between the compared polypeptide sequences. Techniques for determining nucleic acid and amino acid sequence identity also are well known in the art and include determining the nucleotide sequence of
5 the mRNA for that gene (usually via a cDNA intermediate) and determining the amino acid sequence encoded thereby, and comparing this to a second amino acid sequence. In general, "identity" refers to an exact nucleotide to nucleotide or amino acid to amino acid correspondence of
10 two polynucleotides or polypeptide sequences, respectively.

Two or more polynucleotide sequences can be compared by determining their "percent identity." Two or more amino acid sequences likewise can be compared by
15 determining their "percent identity." The percent identity of two sequences, whether nucleic acid or peptide sequences, is generally described as the number of exact matches between two aligned sequences divided by the length of the shorter sequence and multiplied by 100.
20 An approximate alignment for nucleic acid sequences is provided by the local homology algorithm of Smith and Waterman, Advances in Applied Mathematics 2:482-489 (1981). This algorithm can be extended to use with peptide sequences using the scoring matrix developed by
25 Dayhoff, Atlas of Protein Sequences and Structure, M.O. Dayhoff ed., 5 suppl. 3:353-358, National Biomedical Research Foundation, Washington, D.C., USA, and normalized by Gribskov, Nucl. Acids Res. 14(6):6745-6763 (1986). An implementation of this algorithm for nucleic
30 acid and peptide sequences is provided by the Genetics Computer Group (Madison, WI) in their BestFit utility application. The default parameters for this method are

described in the Wisconsin Sequence Analysis Package Program Manual, Version 8 (1995) (available from Genetics Computer Group, Madison, WI). Other equally suitable programs for calculating the percent identity or
5 similarity between sequences are generally known in the art.

For example, percent identity of a particular nucleotide sequence to a reference sequence can be determined using the homology algorithm of Smith and
10 Waterman with a default scoring table and a gap penalty of six nucleotide positions. Another method of establishing percent identity in the context of the present invention is to use the MPSRCH package of programs copyrighted by the University of Edinburgh,
15 developed by John F. Collins and Shane S. Sturrok, and distributed by IntelliGenetics, Inc. (Mountain View, CA). From this suite of packages, the Smith-Waterman algorithm can be employed where default parameters are used for the scoring table (for example, gap open penalty of 12, gap
20 extension penalty of one, and a gap of six). From the data generated, the "Match" value reflects "sequence identity." Other suitable programs for calculating the percent identity or similarity between sequences are generally known in the art, such as the alignment program
25 BLAST, which can also be used with default parameters. For example, BLASTN and BLASTP can be used with the following default parameters: genetic code = standard; filter = none; strand = both; cutoff = 60; expect = 10; Matrix = BLOSUM62; Descriptions = 50 sequences; sort by =
30 HIGH SCORE; Databases = non-redundant, GenBank + EMBL + DDBJ + PDB + GenBank CDS translations + Swiss protein + Spupdate + PIR. Details of these programs can be found at

the following internet address:

<http://www.ncbi.nlm.gov/cgi-bin/BLAST>.

One of skill in the art can readily determine the proper search parameters to use for a given sequence in the above programs. For example, the search parameters may vary based on the size of the sequence in question. Thus, for example, a representative embodiment of the present invention would include an isolated polynucleotide having X contiguous nucleotides, wherein (i) the X contiguous nucleotides have at least about 50% identity to Y contiguous nucleotides derived from any of the sequences described herein, (ii) X equals Y, and (iii) X is greater than or equal to 6 nucleotides and up to 5000 nucleotides, preferably greater than or equal to 8 nucleotides and up to 5000 nucleotides, more preferably 10-12 nucleotides and up to 5000 nucleotides, and even more preferably 15-20 nucleotides, up to the number of nucleotides present in the full-length sequences described herein (e.g., see the Sequence Listing and claims), including all integer values falling within the above-described ranges.

The synthetic expression cassettes (and purified polynucleotides) of the present invention include related polynucleotide sequences having about 80% to 100%, greater than 80-85%, preferably greater than 90-92%, more preferably greater than 95%, and most preferably greater than 98% sequence (including all integer values falling within these described ranges) identity to the synthetic expression cassette sequences disclosed herein (for example, to the sequences presented in Tables 1A and 1B) when the sequences of the present invention are used as the query sequence.

Two nucleic acid fragments are considered to "selectively hybridize" as described herein. The degree of sequence identity between two nucleic acid molecules affects the efficiency and strength of hybridization events between such molecules. A partially identical nucleic acid sequence will at least partially inhibit a completely identical sequence from hybridizing to a target molecule. Inhibition of hybridization of the completely identical sequence can be assessed using hybridization assays that are well known in the art (e.g., Southern blot, Northern blot, solution hybridization, or the like, see Sambrook, et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, (1989) Cold Spring Harbor, N.Y.). Such assays can be conducted using varying degrees of selectivity, for example, using conditions varying from low to high stringency. If conditions of low stringency are employed, the absence of non-specific binding can be assessed using a secondary probe that lacks even a partial degree of sequence identity (for example, a probe having less than about 30% sequence identity with the target molecule), such that, in the absence of non-specific binding events, the secondary probe will not hybridize to the target.

When utilizing a hybridization-based detection system, a nucleic acid probe is chosen that is complementary to a target nucleic acid sequence, and then by selection of appropriate conditions the probe and the target sequence "selectively hybridize," or bind, to each other to form a hybrid molecule. A nucleic acid molecule that is capable of hybridizing selectively to a target sequence under "moderately stringent" typically

hybridizes under conditions that allow detection of a target nucleic acid sequence of at least about 10-14 nucleotides in length having at least approximately 70% sequence identity with the sequence of the selected nucleic acid probe. Stringent hybridization conditions typically allow detection of target nucleic acid sequences of at least about 10-14 nucleotides in length having a sequence identity of greater than about 90-95% with the sequence of the selected nucleic acid probe.

Hybridization conditions useful for probe/target hybridization where the probe and target have a specific degree of sequence identity, can be determined as is known in the art (see, for example, Nucleic Acid Hybridization: A Practical Approach, editors B.D. Hames and S.J. Higgins, (1985) Oxford; Washington, DC; IRL Press).

With respect to stringency conditions for hybridization, it is well known in the art that numerous equivalent conditions can be employed to establish a particular stringency by varying, for example, the following factors: the length and nature of probe and target sequences, base composition of the various sequences, concentrations of salts and other hybridization solution components, the presence or absence of blocking agents in the hybridization solutions (e.g., formamide, dextran sulfate, and polyethylene glycol), hybridization reaction temperature and time parameters, as well as, varying wash conditions. The selection of a particular set of hybridization conditions is selected following standard methods in the art (see, for example, Sambrook, et al., Molecular Cloning: A

Laboratory Manual, Second Edition, (1989) Cold Spring Harbor, N.Y.).

5 A first polynucleotide is "derived from" second polynucleotide if it has the same or substantially the same basepair sequence as a region of the second polynucleotide, its cDNA, complements thereof, or if it displays sequence identity as described above.

10 A first polypeptide is "derived from" a second polypeptide if it is (i) encoded by a first polynucleotide derived from a second polynucleotide, or (ii) displays sequence identity to the second polypeptides as described above.

15 Generally, a viral polypeptide is "derived from" a particular polypeptide of a virus (viral polypeptide) if it is (i) encoded by an open reading frame of a polynucleotide of that virus (viral polynucleotide), or (ii) displays sequence identity to polypeptides of that virus as described above.

20 "Encoded by" refers to a nucleic acid sequence which codes for a polypeptide sequence, wherein the polypeptide sequence or a portion thereof contains an amino acid sequence of at least 3 to 5 amino acids, more preferably at least 8 to 10 amino acids, and even more preferably at least 15 to 20 amino acids from a polypeptide encoded by
25 the nucleic acid sequence. Also encompassed are polypeptide sequences which are immunologically identifiable with a polypeptide encoded by the sequence.

30 "Purified polynucleotide" refers to a polynucleotide of interest or fragment thereof which is essentially free, e.g., contains less than about 50%, preferably less than about 70%, and more preferably less than about 90%, of the protein with which the polynucleotide is naturally associated. Techniques for purifying polynucleotides of interest are well-known in the art and include, for

example, disruption of the cell containing the polynucleotide with a chaotropic agent and separation of the polynucleotide(s) and proteins by ion-exchange chromatography, affinity chromatography and sedimentation according to density.

By "nucleic acid immunization" is meant the introduction of a nucleic acid molecule encoding one or more selected antigens into a host cell, for the *in vivo* expression of an antigen, antigens, an epitope, or epitopes. The nucleic acid molecule can be introduced directly into a recipient subject, such as by injection, inhalation, oral, intranasal and mucosal administration, or the like, or can be introduced *ex vivo*, into cells which have been removed from the host. In the latter case, the transformed cells are reintroduced into the subject where an immune response can be mounted against the antigen encoded by the nucleic acid molecule.

"Gene transfer" or "gene delivery" refers to methods or systems for reliably inserting DNA or RNA of interest into a host cell. Such methods can result in transient expression of non-integrated transferred DNA, extrachromosomal replication and expression of transferred replicons (e.g., episomes), or integration of transferred genetic material into the genomic DNA of host cells. Gene delivery expression vectors include, but are not limited to, vectors derived from bacterial plasmid vectors, viral vectors, non-viral vectors, alphaviruses, pox viruses and vaccinia viruses. When used for immunization, such gene delivery expression vectors may be referred to as vaccines or vaccine vectors.

"T lymphocytes" or "T cells" are non-antibody producing lymphocytes that constitute a part of the cell-mediated arm of the immune system. T cells arise from immature lymphocytes that migrate from the bone marrow to

the thymus, where they undergo a maturation process under the direction of thymic hormones. Here, the mature lymphocytes rapidly divide increasing to very large numbers. The maturing T cells become immunocompetent
5 based on their ability to recognize and bind a specific antigen. Activation of immunocompetent T cells is triggered when an antigen binds to the lymphocyte's surface receptors.

The term "transfection" is used to refer to the
10 uptake of foreign DNA by a cell. A cell has been "transfected" when exogenous DNA has been introduced inside the cell membrane. A number of transfection techniques are generally known in the art. See, e.g., Graham et al. (1973) *Virology*, 52:456, Sambrook et al.
15 (1989) *Molecular Cloning, a laboratory manual*, Cold Spring Harbor Laboratories, New York, Davis et al. (1986) *Basic Methods in Molecular Biology*, Elsevier, and Chu et al. (1981) *Gene* 13:197. Such techniques can be used to introduce one or more exogenous DNA moieties into
20 suitable host cells. The term refers to both stable and transient uptake of the genetic material, and includes uptake of peptide- or antibody-linked DNAs.

A "vector" is capable of transferring gene sequences to target cells (e.g., bacterial plasmid vectors, viral
25 vectors, non-viral vectors, particulate carriers, and liposomes). Typically, "vector construct," "expression vector," and "gene transfer vector," mean any nucleic acid construct capable of directing the expression of a gene of interest and which can transfer gene sequences to
30 target cells. Thus, the term includes cloning and expression vehicles, as well as viral vectors.

Transfer of a "suicide gene" (e.g., a drug-susceptibility gene) to a target cell renders the cell sensitive to compounds or compositions that are

relatively nontoxic to normal cells. Moolten, F.L. (1994) *Cancer Gene Ther.* 1:279-287. Examples of suicide genes are thymidine kinase of herpes simplex virus (HSV-tk), cytochrome P450 (Manome et al. (1996) *Gene Therapy* 3:513-520), human deoxycytidine kinase (Manome et al. (1996) *Nature Medicine* 2(5):567-573) and the bacterial enzyme cytosine deaminase (Dong et al. (1996) *Human Gene Therapy* 7:713-720). Cells which express these genes are rendered sensitive to the effects of the relatively nontoxic prodrugs ganciclovir (HSV-tk), cyclophosphamide (cytochrome P450 2B1), cytosine arabinoside (human deoxycytidine kinase) or 5-fluorocytosine (bacterial cytosine deaminase). Culver et al. (1992) *Science* 256:1550-1552, Huber et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:8302-8306.

A "selectable marker" or "reporter marker" refers to a nucleotide sequence included in a gene transfer vector that has no therapeutic activity, but rather is included to allow for simpler preparation, manufacturing, characterization or testing of the gene transfer vector.

A "specific binding agent" refers to a member of a specific binding pair of molecules wherein one of the molecules specifically binds to the second molecule through chemical and/or physical means. One example of a specific binding agent is an antibody directed against a selected antigen.

By "subject" is meant any member of the subphylum chordata, including, without limitation, humans and other primates, including non-human primates such as chimpanzees and other apes and monkey species; farm animals such as cattle, sheep, pigs, goats and horses; domestic mammals such as dogs and cats; laboratory animals including rodents such as mice, rats and guinea pigs; birds, including domestic, wild and game birds such

as chickens, turkeys and other gallinaceous birds, ducks, geese, and the like. The term does not denote a particular age. Thus, both adult and newborn individuals are intended to be covered. The system described above
5 is intended for use in any of the above vertebrate species, since the immune systems of all of these vertebrates operate similarly.

By "pharmaceutically acceptable" or "pharmacologically acceptable" is meant a material which
10 is not biologically or otherwise undesirable, i.e., the material may be administered to an individual in a formulation or composition without causing any undesirable biological effects or interacting in a deleterious manner with any of the components of the
15 composition in which it is contained.

By "physiological pH" or a "pH in the physiological range" is meant a pH in the range of approximately 7.2 to 8.0 inclusive, more typically in the range of approximately 7.2 to 7.6 inclusive.

20 As used herein, "treatment" refers to any of (i) the prevention of infection or reinfection, as in a traditional vaccine, (ii) the reduction or elimination of symptoms, and (iii) the substantial or complete elimination of the pathogen in question. Treatment may
25 be effected prophylactically (prior to infection) or therapeutically (following infection).

"Lentiviral vector", and "recombinant lentiviral vector" are derived from the subset of retroviral vectors known as lentiviruses. Lentiviral vectors refer to a
30 nucleic acid construct which carries, and within certain embodiments, is capable of directing the expression of a nucleic acid molecule of interest. The lentiviral vector includes at least one transcriptional promoter/enhancer or locus defining element(s), or other elements which

control gene expression by other means such as alternate splicing, nuclear RNA export, post-translational modification of messenger, or post-transcriptional modification of protein. Such vector constructs must
5 also include a packaging signal, long terminal repeats (LTRS) or portion thereof, and positive and negative strand primer binding sites appropriate to the lentiviral vector used (if these are not already present in the retroviral vector). Optionally, the recombinant
10 lentiviral vector may also include a signal which directs polyadenylation, selectable markers such as Neo, TK, hygromycin, phleomycin, histidinol, or DHFR, as well as one or more restriction sites and a translation termination sequence. By way of example, such vectors
15 typically include a 5' LTR, a tRNA binding site, a packaging signal, an origin of second strand DNA synthesis, and a 3' LTR or a portion thereof.

"Lentiviral vector particle" as utilized within the present invention refers to a lentivirus which carries at
20 least one gene of interest. The retrovirus may also contain a selectable marker. The recombinant lentivirus is capable of reverse transcribing its genetic material (RNA) into DNA and incorporating this genetic material into a host cell's DNA upon infection. Lentiviral vector
25 particles may have a lentiviral envelope, a non-lentiviral envelope (e.g., an amphi or VSV-G envelope), or a chimeric envelope.

"Nucleic acid expression vector" or "Expression cassette" refers to an assembly which is capable of
30 directing the expression of a sequence or gene of interest. The nucleic acid expression vector includes a promoter which is operably linked to the sequences or gene(s) of interest. Other control elements may be present as well. Expression cassettes described herein

may be contained within a plasmid construct. In addition to the components of the expression cassette, the plasmid construct may also include a bacterial origin of replication, one or more selectable markers, a signal
5 which allows the plasmid construct to exist as single-stranded DNA (e.g., a M13 origin of replication), a multiple cloning site, and a "mammalian" origin of replication (e.g., a SV40 or adenovirus origin of replication).

10 "Packaging cell" refers to a cell which contains those elements necessary for production of infectious recombinant retrovirus (e.g., lentivirus) which are lacking in a recombinant retroviral vector. Typically, such packaging cells contain one or more expression
15 cassettes which are capable of expressing proteins which encode *Gag*, *pol* and *env* proteins.

"Producer cell" or "vector producing cell" refers to a cell which contains all elements necessary for production of recombinant retroviral vector particles.

20

2. MODES OF CARRYING OUT THE INVENTION

Before describing the present invention in detail, it is to be understood that this invention is not limited to particular formulations or process parameters as such
25 may, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments of the invention only, and is not intended to be limiting.

Although a number of methods and materials similar
30 or equivalent to those described herein can be used in the practice of the present invention, the preferred materials and methods are described herein.

2.1 SYNTHETIC EXPRESSION CASSETTES

2.1.1 MODIFICATION OF HIV-1 GAG NUCLEIC ACID CODING SEQUENCES

One aspect of the present invention is the
5 generation of HIV-1 Gag protein coding sequences, and
related sequences, having improved expression relative to
the corresponding wild-type sequence. An exemplary
embodiment of the present invention is illustrated herein
modifying the Gag protein wild-type sequences obtained
10 from the HIV-1SF2 strain (SEQ ID NO:1; Sanchez-Pescador,
R., et al., *Science* 227(4686): 484-492, 1985; Luciw,
P.A., et al. U.S. Patent No. 5,156,949, issued October
20, 1992; Luciw, P.A., et al., U.S. Patent No. 5,688,688,
November 18, 1997). Gag sequence obtained from other HIV
15 variants may be manipulated in similar fashion following
the teachings of the present specification. Such other
variants include, but are not limited to, Gag protein
encoding sequences obtained from the isolates HIV_{IIIB},
HIV_{SF2}, HIV-
20 1_{SF162}, HIV-1_{SF170}, HIV_{LAV}, HIV_{LAI}, HIV_{MN}, HIV-1_{CM235}, HIV-1_{US4},
other HIV-1 strains from diverse subtypes (e.g.,
subtypes, A through G, and O), HIV-2 strains and diverse
subtypes (e.g., HIV-2_{UC1} and HIV-2_{UC2}), and simian
immunodeficiency virus (SIV). (See, e.g., *Virology*, 3rd
25 Edition (W.K. Joklik ed. 1988); *Fundamental Virology*, 2nd
Edition (B.N. Fields and D.M. Knipe, eds. 1991);
Virology, 3rd Edition (Fields, BN, DM Knipe, PM Howley,
Editors, 1996, Lippincott-Raven, Philadelphia, PA; for a
description of these and other related viruses).

30 First, the HIV-1 codon usage pattern was modified so
that the resulting nucleic acid coding sequence was
comparable to codon usage found in highly expressed human
genes (Example 1). The HIV codon usage reflects a high
content of the nucleotides A or T of the codon-triplet.

The effect of the HIV-1 codon usage is a high AT content in the DNA sequence that results in a decreased translation ability and instability of the mRNA. In comparison, highly expressed human codons prefer the nucleotides G or C. The Gag coding sequences were modified to be comparable to codon usage found in highly expressed human genes. In Figure 11 (Example 1), the percent A-T content of cDNA sequences corresponding to the mRNA for a known unstable mRNA and a known stable mRNA are compared to the percent A-T content of native HIV-1SF2 Gag cDNA and to the synthetic Gag cDNA sequence of the present invention. Experiments performed in support of the present invention showed that the synthetic Gag sequences were capable of higher level of protein production (see the Examples) relative to the native Gag sequences. The data in Figure 11 suggest that one reason for this increased production is increased stability of the mRNA corresponding to the synthetic Gag coding sequences versus the mRNA corresponding to the native Gag coding sequences.

Second, there are inhibitory (or instability) elements (INS) located within the coding sequences of the Gag coding sequences (Example 1). The RRE is a secondary RNA structure that interacts with the HIV encoded Rev-protein to overcome the expression down-regulating effects of the INS. To overcome the post-transcriptional activating mechanisms of RRE and Rev, the instability elements were inactivated by introducing multiple point mutations that did not alter the reading frame of the encoded proteins. Figure 1 shows the original SF2 Gag sequence, the location of the INS sequences, and the modifications made to the INS sequences to reduce their effects. The resulting modified coding sequences are

presented as a synthetic Gag expression cassette (SEQ ID NO:4).

Modification of the Gag polypeptide coding sequences resulted in improved expression relative to the wild-type coding sequences in a number of mammalian cell lines (as well as other types of cell lines, including, but not limited to, insect cells). Further, expression of the sequences resulted in production of virus-like particles (VLPs) by these cell lines (see below). Similar Gag polypeptide coding sequences can be obtained from a variety of isolates (families, sub-types, strains, etc.) including, but not limited to such other variants include, but are not limited to, Gag polypeptide encoding sequences obtained from the isolates HIV_{IIIB}, HIV_{SF2}, HIV-1_{SF162}, HIV-1_{SF170}, HIV_{LAV}, HIV_{LAI}, HIV_{MN}, HIV-1_{CM235}, HIV-1_{US4}, other HIV-1 strains from diverse subtypes (e.g., subtypes, A through G, and O), HIV-2 strains and diverse subtypes (e.g., HIV-2_{UC1} and HIV-2_{UC2}), and simian immunodeficiency virus (SIV). (See, e.g., Virology, 3rd Edition (W.K. Joklik ed. 1988); *Fundamental Virology*, 2nd Edition (B.N. Fields and D.M. Knipe, eds. 1991; *Virology*, 3rd Edition (Fields, BN, DM Knipe, PM Howley, Editors, 1996, Lippincott-Raven, Philadelphia, PA). Gag polypeptide encoding sequences derived from these variants can be optimized and tested for improved expression in mammals by following the teachings of the present specification (see the Examples, in particular Example 1).

2.1.2 FURTHER MODIFICATION OF SEQUENCES INCLUDING HIV-1 GAG NUCLEIC ACID CODING SEQUENCES

Experiments performed in support of the present invention have shown that similar modifications of HIV-1 Gag-protease, Gag-reverse transcriptase and Gag-polymerase sequences also result in improved expression

of the polyproteins, as well as, the production of VLPs formed by polypeptides produced from such modified coding sequences.

For the Gag-protease sequence (wild type, SEQ ID NO:2; modified, SEQ ID NOs:5, 78, 79), the changes in codon usage were restricted to the regions upstream of the -1 frameshift (Figure 2). Further, inhibitory (or instability) elements (INS) located within the coding sequences of the Gag-protease polypeptide coding sequence were altered as well (indicated in Figure 2). Exemplary constructs (which include the -1 frameshift) encoding modified Gag-protease sequences include those shown in SEQ ID NOs:78 and 79 (Figures 69 and 70). These are: GP1 (SEQ ID NO:78) in which the protease region was also codon optimized and INS inactivated and GP2 (SEQ ID NO:79), in which the protease region was only subjected to INS inactivation.

For other Gag-containing sequences, for example the Gag-polymerase sequence (wild type, SEQ ID NO:3; modified, SEQ ID NO:6) or Gag-reverse transcriptase (wild type, SEQ ID NO:77; modified SEQ ID NOs:80-84), the changes in codon usage are similar to those for the Gag-protease sequence. Those expression cassettes which contain a frameshift in the GagPol coding sequence are designated "FS(+)" (SEQ ID NOs:80 and 81, Figures 71 and 72) while the designation "FS(-)" (SEQ ID Nos: 82, 83 and 84, Figures 73, 74 and 75) indicates that there is no frameshift utilized in this coding sequence.

In addition to polyproteins containing HIV-related sequences, the various Gag-, Gag-prot, Gag-pol, Gag-reverse transcriptase encoding sequences of the present invention can be fused to other polypeptides (creating chimeric polypeptides) for which an immunogenic response is desired. An example of such a chimeric protein is the

joining of the improved expression Gag encoding sequences to the Hepatitis C Virus (HCV) core protein. In this case, the HCV-core encoding sequences were placed in-frame with the HIV-Gag encoding sequences, resulting in the Gag/HCV-core encoding sequence presented as SEQ ID NO:7 (wild type sequence presented as SEQ ID NO:8).

Further sequences useful in the practice of the present invention include, but are not limited to, sequences encoding viral epitopes/antigens {including but not limited to, HCV antigens (e.g., E1, E2; Houghton, M., et al., U.S. Patent No. 5,714,596, issued February 3, 1998; Houghton, M., et al., U.S. Patent No. 5,712,088, issued January 27, 1998; Houghton, M., et al., U.S. Patent No. 5,683,864, issued November 4, 1997; Weiner, A.J., et al., U.S. Patent No. 5,728,520, issued March 17, 1998; Weiner, A.J., et al., U.S. Patent No. 5,766,845, issued June 16, 1998; Weiner, A.J., et al., U.S. Patent No. 5,670,152, issued September 23, 1997), HIV antigens (e.g., derived from *nef*, *tat*, *rev*, *vpu*, *vif*, *vpr* and/or *env*); and sequences encoding tumor antigens/epitopes. Additional sequences are described below. Also, variations on the orientation of the Gag and other coding sequences, relative to each other, are also described below.

Gag, Gag-protease, Gag-reverse transcriptase and/or Gag-polymerase polypeptide coding sequences can be obtained from any HIV isolates (different families, subtypes, and strains) including but not limited to the isolates HIV_{IIIB}, HIV_{SF2}, HIV_{SF162}, HIV_{US4}, HIV_{CM235}, HIV_{LAV}, HIV_{LAI}, HIV_{MN} (see, e.g., Myers et al. Los Alamos Database, Los Alamos National Laboratory, Los Alamos, New Mexico (1992); Myers et al., *Human Retroviruses and Aids*, 1997, Los Alamos, New Mexico: Los Alamos National Laboratory). Synthetic expression cassettes can be generated using

such coding sequences as starting material by following the teachings of the present specification (e.g., see Example 1). Further, the synthetic expression cassettes of the present invention include related Gag polypeptide coding sequences having greater than 75%, preferably greater than 80-85%, more preferably greater than 90-95%, and most preferably greater than 98% sequence identity (or any integer value within these ranges) to the synthetic expression cassette sequences disclosed herein (for example, SEQ ID NO:4; SEQ ID NO:5; SEQ ID NO:6; and SEQ ID NO:20, the Gag Major Homology Region).

2.1.3 EXPRESSION OF SYNTHETIC SEQUENCES ENCODING HIV-1 GAG AND RELATED POLYPEPTIDES

Several synthetic Gag-encoding sequences (expression cassettes) of the present invention were cloned into a number of different expression vectors (Example 1) to evaluate levels of expression and production of VLPs. Two modified synthetic coding sequences are presented as a synthetic Gag expression cassette (SEQ ID NO:4) and a synthetic Gag-protease expression cassette (SEQ ID NOs:78 and 79). Other synthetic Gag-encoding proteins are presented, for example, as SEQ ID NOs:80 through 84. The synthetic DNA fragments for Gag-encoding polypeptides (e.g., Gag, Gag-protease, Gag-polymerase, Gag-reverse transcriptase) were cloned into expression vectors described in Example 1, including, a transient expression vector, CMV-promoter-based mammalian vectors, and a shuttle vector for use in baculovirus expression systems. Corresponding wild-type sequences were cloned into the same vectors.

These vectors were then transfected into a several different cell types, including a variety of mammalian

cell lines, (293, RD, COS-7, and CHO, cell lines available, for example, from the A.T.C.C.). The cell lines were cultured under appropriate conditions and the levels of p24 (Gag) expression in supernatants were
5 evaluated (Example 2). The results of these assays demonstrated that expression of synthetic Gag-encoding sequences were significantly higher than corresponding wild-type sequences (Example 2; Table 2).

Further, Western Blot analysis showed that cells
10 containing the synthetic Gag expression cassette produced the expected 55 kD (p55) protein at higher per-cell concentrations than cells containing the native expression cassette. The Gag p55 protein was seen in both cell lysates and supernatants. The levels of
15 production were significantly higher in cell supernatants for cells transfected with the synthetic Gag expression cassette of the present invention. Experiments performed in support of the present invention suggest that cells containing the synthetic Gag-prot expression cassettes
20 produced the expected Gag-prot protein at comparably higher per-cell concentrations than cells containing the wild-type expression cassette.

Fractionation of the supernatants from mammalian cells transfected with the synthetic Gag expression
25 cassette showed that it provides superior production of both p55 protein and VLPs, relative to the wild-type Gag sequences (Examples 6 and 7).

Efficient expression of these Gag-containing polypeptides in mammalian cell lines provides the
30 following benefits: the Gag polypeptides are free of baculovirus contaminants; production by established methods approved by the FDA; increased purity; greater yields (relative to native coding sequences); and a novel method of producing the Gag-containing polypeptides in

CHO or other mammalian cells which is not feasible in the absence of the increased expression obtained using the constructs of the present invention. Exemplary Mammalian cell lines include, but are not limited to, BHK, VERO, HT1080, 293, 293T, RD, COS-7, CHO, Jurkat, HUT, SUPT, C8166, MOLT4/clone8, MT-2, MT-4, H9, PM1, CEM, myeloma cells (e.g., SB20 cells) and CEMX174, such cell lines are available, for example, from the A.T.C.C.).

A synthetic Gag expression cassette of the present invention also demonstrated high levels of expression and VLP production when transfected into insect cells (Example 7). Further, in addition to a higher total protein yield, the final product from the synthetic p55-expressed Gag consistently contained lower amounts of contaminating baculovirus proteins than the final purified product from the native p55-expressed Gag.

Further, synthetic Gag expression cassettes of the present invention have also been introduced into yeast vectors which were transformed into and efficiently expressed by yeast cells (*Saccharomyces cerevisiae*; using vectors as described in Rosenberg, S. and Tekamp-Olson, P., U.S. Patent No. RE35,749, issued, March 17, 1998).

In addition to the mammalian and insect vectors described in the Examples, the synthetic expression cassettes of the present invention can be incorporated into a variety of expression vectors using selected expression control elements. Appropriate vectors and control elements for any given cell type can be selected by one having ordinary skill in the art in view of the teachings of the present specification and information known in the art about expression vectors.

For example, a synthetic Gag expression cassette can be inserted into a vector which includes control elements operably linked to the desired coding sequence, which

allow for the expression of the gene in a selected cell-type. For example, typical promoters for mammalian cell expression include the SV40 early promoter, a CMV promoter such as the CMV immediate early promoter (a CMV promoter can include intron A), RSV, HIV-LTR, the mouse mammary tumor virus LTR promoter (MMLV-LTR), FIV-LTR, the adenovirus major late promoter (Ad MLP), and the herpes simplex virus promoter, among others. Other nonviral promoters, such as a promoter derived from the murine metallothionein gene, will also find use for mammalian expression. Typically, transcription termination and polyadenylation sequences will also be present, located 3' to the translation stop codon. Preferably, a sequence for optimization of initiation of translation, located 5' to the coding sequence, is also present. Examples of transcription terminator/polyadenylation signals include those derived from SV40, as described in Sambrook, et al., *supra*, as well as a bovine growth hormone terminator sequence. Introns, containing splice donor and acceptor sites, may also be designed into the constructs for use with the present invention (Chapman et al., *Nuc. Acids Res.* (1991) 19:3979-3986).

Enhancer elements may also be used herein to increase expression levels of the mammalian constructs. Examples include the SV40 early gene enhancer, as described in Dijkema et al., *EMBO J.* (1985) 4:761, the enhancer/promoter derived from the long terminal repeat (LTR) of the Rous Sarcoma Virus, as described in Gorman et al., *Proc. Natl. Acad. Sci. USA* (1982b) 79:6777 and elements derived from human CMV, as described in Boshart et al., *Cell* (1985) 41:521, such as elements included in the CMV intron A sequence (Chapman et al., *Nuc. Acids Res.* (1991) 19:3979-3986).

The desired synthetic Gag polypeptide encoding sequences can be cloned into any number of commercially available vectors to generate expression of the polypeptide in an appropriate host system. These systems include, but are not limited to, the following:

5 baculovirus expression {Reilly, P.R., et al., BACULOVIRUS EXPRESSION VECTORS: A LABORATORY MANUAL (1992); Beames, et al., *Biotechniques* 11:378 (1991); Pharmingen; Clontech, Palo Alto, CA)}, vaccinia expression {Earl, P. L., et al.,

10 "Expression of proteins in mammalian cells using vaccinia" In *Current Protocols in Molecular Biology* (F. M. Ausubel, et al. Eds.), Greene Publishing Associates & Wiley Interscience, New York (1991); Moss, B., et al., U.S. Patent Number 5,135,855, issued 4 August 1992},

15 expression in bacteria {Ausubel, F.M., et al., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley and Sons, Inc., Media PA; Clontech}, expression in yeast {Rosenberg, S. and Tekamp-Olson, P., U.S. Patent No. RE35,749, issued, March 17, 1998; Shuster, J.R., U.S. Patent No. 5,629,203,

20 issued May 13, 1997; Gellissen, G., et al., *Antonie Van Leeuwenhoek*, 62(1-2):79-93 (1992); Romanos, M.A., et al., *Yeast* 8(6):423-488 (1992); Goeddel, D.V., *Methods in Enzymology* 185 (1990); Guthrie, C., and G.R. Fink, *Methods in Enzymology* 194 (1991)}, expression in

25 mammalian cells {Clontech; Gibco-BRL, Ground Island, NY; e.g., Chinese hamster ovary (CHO) cell lines (Haynes, J., et al., *Nuc. Acid. Res.* 11:687-706 (1983); 1983, Lau, Y.F., et al., *Mol. Cell. Biol.* 4:1469-1475 (1984); Kaufman, R. J., "Selection and coamplification of

30 heterologous genes in mammalian cells," in *Methods in Enzymology*, vol. 185, pp537-566. Academic Press, Inc., San Diego CA (1991)}, and expression in plant cells {plant cloning vectors, Clontech Laboratories, Inc., Palo Alto, CA, and Pharmacia LKB Biotechnology, Inc.,

Piscataway, NJ; Hood, E., et al., *J. Bacteriol.* 168:1291-1301 (1986); Nagel, R., et al., *FEMS Microbiol. Lett.* 67:325 (1990); An, et al., "Binary Vectors", and others in Plant Molecular Biology Manual A3:1-19 (1988);
5 Miki, B.L.A., et al., pp.249-265, and others in Plant DNA Infectious Agents (Hohn, T., et al., eds.) Springer-Verlag, Wien, Austria, (1987); *Plant Molecular Biology: Essential Techniques*, P.G. Jones and J.M. Sutton, New York, J. Wiley, 1997; Miglani, Gurbachan *Dictionary of*
10 *Plant Genetics and Molecular Biology*, New York, Food Products Press, 1998; Henry, R. J., *Practical Applications of Plant Molecular Biology*, New York, Chapman & Hall, 1997}.

Also included in the invention is an expression
15 vector, such as the CMV promoter-containing vectors described in Example 1, containing coding sequences and expression control elements which allow expression of the coding regions in a suitable host. The control elements generally include a promoter, translation initiation
20 codon, and translation and transcription termination sequences, and an insertion site for introducing the insert into the vector. Translational control elements have been reviewed by M. Kozak (e.g., Kozak, M., *Mamm. Genome* 7(8):563-574, 1996; Kozak, M., *Biochimie*
25 76(9):815-821, 1994; Kozak, M., *J Cell Biol* 108(2):229-241, 1989; Kozak, M., and Shatkin, A.J., *Methods Enzymol* 60:360-375, 1979).

Expression in yeast systems has the advantage of commercial production. Recombinant protein production by
30 vaccinia and CHO cell line have the advantage of being mammalian expression systems. Further, vaccinia virus expression has several advantages including the following: (i) its wide host range; (ii) faithful post-

transcriptional modification, processing, folding, transport, secretion, and assembly of recombinant proteins; (iii) high level expression of relatively soluble recombinant proteins; and (iv) a large capacity to accommodate foreign DNA.

The recombinantly expressed polypeptides from synthetic Gag-encoding expression cassettes are typically isolated from lysed cells or culture media. Purification can be carried out by methods known in the art including salt fractionation, ion exchange chromatography, gel filtration, size-exclusion chromatography, size-fractionation, and affinity chromatography.

Immunoaffinity chromatography can be employed using antibodies generated based on, for example, Gag antigens.

Advantages of expressing the Gag-containing proteins of the present invention using mammalian cells include, but are not limited to, the following: well-established protocols for scale-up production; the ability to produce VLPs; cell lines are suitable to meet good manufacturing process (GMP) standards; culture conditions for mammalian cells are known in the art.

2.1.4 MODIFICATION OF HIV-1 ENV NUCLEIC ACID CODING SEQUENCES

One aspect of the present invention is the generation of HIV-1 Env protein coding sequences, and related sequences, having improved expression relative to the corresponding wild-type sequence. Exemplary embodiments of the present invention are illustrated herein modifying the Env protein wild-type sequences obtained from the HIV-1 subtype B strains HIV-1US4 and HIV-1SF162 (Myers et al., Los Alamos Database, Los Alamos National Laboratory, Los Alamos, New Mexico (1992); Myers et al., *Human Retroviruses and Aids*, 1997, Los Alamos,

New Mexico: Los Alamos National Laboratory). Env sequence obtained from other HIV variants may be manipulated in similar fashion following the teachings of the present specification. Such other variants include those
5 described above in Section 2.1.1 and on the World Wide Web (Internet), for example at <http://hiv-web.lanl.gov/cgi-bin/hivDB3/public/wdb/ssampublic> and <http://hiv-web.lanl.gov>.

First, the HIV-1 codon usage pattern was modified so
10 that the resulting nucleic acid coding sequence was comparable to codon usage found in highly expressed human genes (Example 1). The HIV codon usage reflects a high content of the nucleotides A or T of the codon-triplet. The effect of the HIV-1 codon usage is a high AT content
15 in the DNA sequence that results in a decreased translation ability and instability of the mRNA. In comparison, highly expressed human codons prefer the nucleotides G or C. The Env coding sequences were modified to be comparable to codon usage found in highly
20 expressed human genes. Experiments performed in support of the present invention showed that the synthetic Env sequences were capable of higher level of protein production (see the Examples) relative to the native Env sequences. One reason for this increased production may
25 be increased stability of the mRNA corresponding to the synthetic Env coding sequences versus the mRNA corresponding to the native Env coding sequences.

Modification of the Env polypeptide coding sequences resulted in improved expression relative to the wild-type
30 coding sequences in a number of mammalian cell lines. Similar Env polypeptide coding sequences can be obtained from a variety of isolates (families, sub-types, etc.). Env polypeptide encoding sequences derived from these variants can be optimized and tested for improved

expression in mammals by following the teachings of the present specification (see the Examples, in particular Example 2).

5 2.1.5 FURTHER MODIFICATION OF HIV-1 ENV NUCLEIC ACID
 CODING SEQUENCES

 In addition to proteins containing HIV-related sequences, the Env encoding sequences of the present invention can be fused to other polypeptides (creating
10 chimeric polypeptides). Also, variations on the orientation of the Env and other coding sequences, relative to each other, are contemplated. Further, the HIV protein encoding cassettes of the present invention can be co-expressed using one vector or multiple vectors.
15 In addition, the polyproteins can be operably linked to the same or different promoters.

 Env polypeptide coding sequences can be obtained from any HIV isolates (different families, subtypes, and strains) including but not limited to the isolates HIV_{IIIB},
20 HIV_{SF2}, HIV_{US4}, HIV_{CM235}, HIV_{SF162}, HIV_{LAV}, HIV_{LAI}, HIV_{MN}) (see, e.g., Myers et al., Los Alamos Database, Los Alamos National Laboratory, Los Alamos, New Mexico (1992); Myers et al., *Human Retroviruses and Aids*, 1997, Los Alamos, New Mexico: Los Alamos National Laboratory). Synthetic
25 expression cassettes can be generated using such coding sequences as starting material by following the teachings of the present specification (e.g., see Example 1). Further, the synthetic expression cassettes (and purified polynucleotides) of the present invention include related
30 Env polypeptide coding sequences having greater than 90%, preferably greater than 92%, more preferably greater than 95%, and most preferably greater than 98% sequence identity to the synthetic expression cassette sequences disclosed herein (for example, SEQ ID NOS:71-72; and/or

the sequences presented in Tables 1A and 1B) when the sequences of the present invention are used as the query sequence.

5 2.1.6 **EXPRESSION OF SYNTHETIC SEQUENCES ENCODING HIV-1
 ENV AND RELATED POLYPEPTIDES**

Several synthetic Env-encoding sequences (expression cassettes) of the present invention were cloned into a number of different expression vectors (Example 1) to
10 evaluate levels of expression and production of Env polypeptide. A modified synthetic coding sequence is presented as synthetic Env expression cassettes (Example 1, e.g., Tables 1A and 1B). The synthetic DNA fragments for Env were cloned into eucaryotic expression vectors
15 described in Example 1 and in Section 2.1.3 above, including, a transient expression vector and CMV-promoter-based mammalian vectors. Corresponding wild-type sequences were cloned into the same vectors.

These vectors were then transfected into a several
20 different cell types, including a variety of mammalian cell lines, (293, RD, COS-7, and CHO, cell lines available, for example, from the A.T.C.C.). The cell lines were cultured under appropriate conditions and the levels of gp120, gp140 and gp160 Env expression in
25 supernatants were evaluated (Example 2). Env polypeptides include, but are not limited to, for example, native gp160, oligomeric gp140, monomeric gp120 as well as modified sequences of these polypeptides. The results of these assays demonstrated that expression of
30 synthetic Env encoding sequences were significantly higher than corresponding wild-type sequences (Example 2; Tables 3 and 4).

Further, Western Blot analysis showed that cells containing the synthetic Env expression cassette produced

the expected protein (gp120, gp140 or gp160) at higher per-cell concentrations than cells containing the native expression cassette. The Env proteins were seen in both cell lysates and supernatants. The levels of production
5 were significantly higher in cell supernatants for cells transfected with the synthetic Env expression cassettes of the present invention as compared to wild type.

Fractionation of the supernatants from mammalian cells transfected with the synthetic Env expression
10 cassettes showed that it provides superior production of Env proteins, relative to the wild-type Env sequences (Examples 2 and 3).

Efficient expression of these Env-containing polypeptides in mammalian cell lines provides the
15 following benefits: the Env polypeptides are free of baculovirus or other viral contaminants; production by established methods approved by the FDA; increased purity; greater yields (relative to native coding sequences); and a novel method of producing the Env-
20 containing polypeptides in CHO cells which is less feasible in the absence of the increased expression obtained using the constructs of the present invention.

Exemplary cell lines (e.g., mammalian, yeast, insect, etc.) include those described above in Section
25 2.1.3 for Gag-containing constructs. Further, appropriate vectors and control elements (e.g., promoters, enhancers, polyadenylation sequences, etc.) for any given cell type can be selected, as described above in Section 2.1.3, by one having ordinary skill in the art in view of the
30 teachings of the present specification and information known in the art about expression vectors. In addition, the recombinantly expressed polypeptides from synthetic Env-encoding expression cassettes are typically isolated and purified from lysed cells or culture media, as

described above for Gag-encoding expression cassettes. An exemplary purification is described in Example 4 and shown in Figure 60.

5 2.1.7 MODIFICATION OF HIV-1 TAT NUCLEIC ACID CODING
SEQUENCES

Another aspect of the present invention is the generation of HIV-1 tat protein coding sequences, and related sequences, having improved expression relative to
10 the corresponding wild-type sequence. Exemplary embodiments of the present invention are illustrated herein modifying the tat wild-type nucleotide sequence (SEQ ID NO:85, Figure 76) obtained from SF162 as described above. Exemplary synthetic tat constructs are
15 shown in SEQ ID NO:87, which depicts a tat construct encoding a full-length tat polypeptide from strain SF162; SEQ ID NO:88, which depicts a tat construct encoding a tat polypeptide having the cystein residue at position 22 changed; and SEQ ID NO:89, which depicts a tat construct
20 encoding the amino terminal portion of a tat polypeptide from strain SF162. The amino portion of the tat protein appears to contain many of the epitopes that induce an immune response. In addition, further modifications include replacement or deletion of the cystein residue at
25 position 22, for example with a valine residue, an alanine residue or a glycine residue (SEQ ID Nos: 88 and 89, Figures 79 and 81), see, e.g., Caputo et al. (1996) *Gene Ther.* 3:235. In Figure 81, which depicts a tat construct encoding the amino terminal portion of a tat
30 polypeptide, the nucleotides (nucleotides 64-66) encoding the cystein residues are underlined. The design and construction of suitable construct can be readily done using

the teachings of the present specification. As with Gag, pol, prot and Env, tat polypeptide coding sequences can be obtained from a variety of isolates (families, subtypes, etc.).

5 Modification of the tat polypeptide coding sequences result in improved expression relative to the wild-type coding sequences in a number of cell lines (e.g., mammalian, yeast, bacterial and insect cells). Tat polypeptide encoding sequences derived from these
10 variants can be optimized and tested for improved expression in mammals by following the teachings of the present specification (see the Examples, in particular Example 2).

 Various forms of the different embodiments of the
15 invention, described herein, may be combined. For example, polynucleotides may be derived from the polynucleotide sequences of the present invention, including, but not limited to, coding sequences for Gag polypeptides, Env polypeptides, polymerase polypeptides,
20 protease polypeptides, tat polypeptides, and reverse transcriptase polypeptides. Further, the polynucleotide coding sequences of the present invention may be combined into multi-cistronic expression cassettes where typically each coding sequence for each polypeptide is preceded by
25 IRES sequences.

2.2 PRODUCTION OF VIRUS-LIKE PARTICLES AND USE OF THE CONSTRUCTS OF THE PRESENT INVENTION TO CREATE PACKAGING CELL LINES

30 The group-specific antigens (Gag) of human immunodeficiency virus type-1 (HIV-1) self-assemble into noninfectious virus-like particles (VLP) that are released from various eucaryotic cells by budding (reviewed by Freed, E.O., *Virology* 251:1-15, 1998). The

synthetic expression cassettes of the present invention provide efficient means for the production of HIV-Gag virus-like particles (VLPs) using a variety of different cell types, including, but not limited to, mammalian
5 cells.

Viral particles can be used as a matrix for the proper presentation of an antigen entrapped or associated therewith to the immune system of the host. For example, U.S. Patent No. 4,722,840 describes hybrid particles
10 comprised of a particle-forming fragment of a structural protein from a virus, such as a particle-forming fragment of hepatitis B virus (HBV) surface antigen (HBsAg), fused to a heterologous polypeptide. Tindle et al., *Virology* (1994) 200:547-557, describes the production and use of
15 chimeric HBV core antigen particles containing epitopes of human papillomavirus (HPV) type 16 E7 transforming protein.

Adams et al., *Nature* (1987) 329:68-70, describes the recombinant production of hybrid HIVgp120:Ty VLPs in
20 yeast and Brown et al., *Virology* (1994) 198:477-488, the production of chimeric proteins consisting of the VP2 protein of human parvovirus B19 and epitopes from human herpes simplex virus type 1, as well as mouse hepatitis virus A59. Wagner et al., (*Virology* (1994) 200:162-175,
25 Brand et al., *J. Virol. Meth.* (1995) 51:153-168; *Virology* (1996) 220:128-140) and Wolf, et al., (EP 0 449 116 A1, published 2 October 1991; WO 96/30523, published 3
October 1996) describe the assembly of chimeric HIV-1 p55Gag particles. U.S. Patent No. 5,503,833 describes
30 the use of rotavirus VP6 spheres for encapsulating and delivering therapeutic agents.

2.2.1 VLP PRODUCTION USING THE SYNTHETIC EXPRESSION CASSETTES OF THE PRESENT INVENTION

Experiments performed in support of the present invention have demonstrated that the synthetic expression
5 cassettes of the present invention provide superior production of both protein and VLPs, relative to native coding sequences (Examples 7 and 15). Further, electron microscopic evaluation of VLP production (Examples 6 and 15, Figures 3A-B and 65A-F) showed that free and budding
10 immature virus particles of the expected size were produced by cells containing the synthetic expression cassettes.

Using the synthetic expression cassettes of the present invention, rather than native coding sequences,
15 for the production of virus-like particles provide several advantages. First, VLPs can be produced in enhanced quantity making isolation and purification of the VLPs easier. Second, VLPs can be produced in a variety of cell types using the synthetic expression
20 cassettes, in particular, mammalian cell lines can be used for VLP production, for example, CHO cells. Production using CHO cells provides (i) VLP formation; (ii) correct myristylation and budding; (iii) absence of non-mammalian cell contaminants (e.g., insect viruses
25 and/or cells); and (iv) ease of purification. The synthetic expression cassettes of the present invention are also useful for enhanced expression in cell-types other than mammalian cell lines. For example, infection of insect cells with baculovirus vectors encoding the
30 synthetic expression cassettes resulted in higher levels of total protein yield and higher levels of VLP production (relative to wild-type coding sequences). Further, the final product from insect cells infected with the baculovirus-Gag synthetic expression cassettes

consistently contained lower amounts of contaminating insect proteins than the final product when wild-type coding sequences were used (Examples).

5 VLPs can spontaneously form when the particle-forming polypeptide of interest is recombinantly expressed in an appropriate host cell. Thus, the VLPs produced using the synthetic expression cassettes of the present invention are conveniently prepared using recombinant techniques. As discussed below, the Gag
10 polypeptide encoding synthetic expression cassettes of the present invention can include other polypeptide coding sequences of interest (for example, Env, tat, rev, HIV protease, HIV polymerase, HCV core; see, Example 1). Expression of such synthetic expression cassettes yields
15 VLPs comprising the product of the synthetic expression cassette, as well as, the polypeptide of interest.

Once coding sequences for the desired particle-forming polypeptides have been isolated or synthesized, they can be cloned into any suitable vector or replicon
20 for expression. Numerous cloning vectors are known to those of skill in the art, and the selection of an appropriate cloning vector is a matter of choice. See, generally, Ausubel et al, *supra* or Sambrook et al, *supra*. The vector is then used to transform an appropriate host
25 cell. Suitable recombinant expression systems include, but are not limited to, bacterial, mammalian, baculovirus/insect, vaccinia, Semliki Forest virus (SFV), Alphaviruses (such as, Sindbis, Venezuelan Equine Encephalitis (VEE)), mammalian, yeast and Xenopus
30 expression systems, well known in the art. Particularly preferred expression systems are mammalian cell lines, vaccinia, Sindbis, insect and yeast systems.

For example, a number of mammalian cell lines are known in the art and include immortalized cell lines

available from the American Type Culture Collection (A.T.C.C.), such as, but not limited to, Chinese hamster ovary (CHO) cells, 293 cells, HeLa cells, baby hamster kidney (BHK) cells, mouse myeloma (SB20), monkey kidney cells (COS), as well as others. Similarly, bacterial hosts such as *E. coli*, *Bacillus subtilis*, and *Streptococcus spp.*, will find use with the present expression constructs. Yeast hosts useful in the present invention include *inter alia*, *Saccharomyces cerevisiae*, *Candida albicans*, *Candida maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis*, *Kluyveromyces lactis*, *Pichia guilliermondii*, *Pichia pastoris*, *Schizosaccharomyces pombe* and *Yarrowia lipolytica*. Insect cells for use with baculovirus expression vectors include, *inter alia*, *Aedes aegypti*, *Autographa californica*, *Bombyx mori*, *Drosophila melanogaster*, *Spodoptera frugiperda*, and *Trichoplusia ni*. See, e.g., Summers and Smith, *Texas Agricultural Experiment Station Bulletin No. 1555* (1987). Fungal hosts include, for example, *Aspergillus*.

Viral vectors can be used for the production of particles in eucaryotic cells, such as those derived from the pox family of viruses, including vaccinia virus and avian poxvirus. Additionally, a vaccinia based infection/transfection system, as described in Tomei et al., *J. Virol.* (1993) 67:4017-4026 and Selby et al., *J. Gen. Virol.* (1993) 74:1103-1113, will also find use with the present invention. In this system, cells are first infected *in vitro* with a vaccinia virus recombinant that encodes the bacteriophage T7 RNA polymerase. This polymerase displays exquisite specificity in that it only transcribes templates bearing T7 promoters. Following infection, cells are transfected with the DNA of interest, driven by a T7 promoter. The polymerase expressed in the cytoplasm from the vaccinia virus

recombinant transcribes the transfected DNA into RNA which is then translated into protein by the host translational machinery. Alternately, T7 can be added as a purified protein or enzyme as in the "Progenitor" system (Studier and Moffatt, *J. Mol. Biol.* (1986) 189:113-130). The method provides for high level, transient, cytoplasmic production of large quantities of RNA and its translation product(s).

Depending on the expression system and host selected, the VLPs are produced by growing host cells transformed by an expression vector under conditions whereby the particle-forming polypeptide is expressed and VLPs can be formed. The selection of the appropriate growth conditions is within the skill of the art. If the VLPs are formed intracellularly, the cells are then disrupted, using chemical, physical or mechanical means, which lyse the cells yet keep the VLPs substantially intact. Such methods are known to those of skill in the art and are described in, e.g., *Protein Purification Applications: A Practical Approach*, (E.L.V. Harris and S. Angal, Eds., 1990).

The particles are then isolated (or substantially purified) using methods that preserve the integrity thereof, such as, by density gradient centrifugation, e.g., sucrose gradients, PEG-precipitation, pelleting, and the like (see, e.g., Kirnbauer et al. *J. Virol.* (1993) 67:6929-6936), as well as standard purification techniques including, e.g., ion exchange and gel filtration chromatography.

VLPs produced by cells containing the synthetic expression cassettes of the present invention can be used to elicit an immune response when administered to a subject. One advantage of the present invention is that VLPs can be produced by mammalian cells carrying the

synthetic expression cassettes at levels previously not possible. As discussed above, the VLPs can comprise a variety of antigens in addition to the Gag polypeptides (e.g., Env, tat, Gag-protease, Gag-polymerase, Gag-HCV-core). Purified VLPs, produced using the synthetic expression cassettes of the present invention, can be administered to a vertebrate subject, usually in the form of vaccine compositions. Combination vaccines may also be used, where such vaccines contain, for example, other subunit proteins derived from HIV or other organisms (e.g., env) or gene delivery vaccines encoding such antigens. Administration can take place using the VLPs formulated alone or formulated with other antigens. Further, the VLPs can be administered prior to, concurrent with, or subsequent to, delivery of the synthetic expression cassettes for DNA immunization (see below) and/or delivery of other vaccines. Also, the site of VLP administration may be the same or different as other vaccine compositions that are being administered. Gene delivery can be accomplished by a number of methods including, but are not limited to, immunization with DNA, alphavirus vectors, pox virus vectors, and vaccinia virus vectors.

VLP immune-stimulating (or vaccine) compositions can include various excipients, adjuvants, carriers, auxiliary substances, modulating agents, and the like. The immune stimulating compositions will include an amount of the VLP/antigen sufficient to mount an immunological response. An appropriate effective amount can be determined by one of skill in the art. Such an amount will fall in a relatively broad range that can be determined through routine trials and will generally be an amount on the order of about 0.1 μ g to about 1000 μ g,

more preferably about 1 μ g to about 300 μ g, of VLP/antigen.

A carrier is optionally present which is a molecule that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycollic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or liposomes), and inactive virus particles. Examples of particulate carriers include those derived from polymethyl methacrylate polymers, as well as microparticles derived from poly(lactides) and poly(lactide-co-glycolides), known as PLG. See, e.g., Jeffery et al., *Pharm. Res.* (1993) 10:362-368; McGee JP, et al., *J Microencapsul.* 14(2):197-210, 1997; O'Hagan DT, et al., *Vaccine* 11(2):149-54, 1993. Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents ("adjuvants"). Furthermore, the antigen may be conjugated to a bacterial toxoid, such as toxoid from diphtheria, tetanus, cholera, etc., as well as toxins derived from *E. coli*.

Such adjuvants include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc.; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59 (International Publication No. WO 90/14837), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated

into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA), (b) SAF, containing 10% Squalane, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) Ribⁱ™ adjuvant system (RAS), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (Detox™); (3) saponin adjuvants, such as Stimulon™ (Cambridge Bioscience, Worcester, MA) may be used or particle generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (IL-1, IL-2, etc.), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), beta chemokines (MIP, 1-alpha, 1-beta Rantes, etc.); (6) detoxified mutants of a bacterial ADP-ribosylating toxin such as a cholera toxin (CT), a pertussis toxin (PT), or an *E. coli* heat-labile toxin (LT), particularly LT-K63 (where lysine is substituted for the wild-type amino acid at position 63) LT-R72 (where arginine is substituted for the wild-type amino acid at position 72), CT-S109 (where serine is substituted for the wild-type amino acid at position 109), and PT-K9/G129 (where lysine is substituted for the wild-type amino acid at position 9 and glycine substituted at position 129) (see, e.g., International Publication Nos. W093/13202 and W092/19265); and (7)

other substances that act as immunostimulating agents to enhance the effectiveness of the composition.

Muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acteyl-normuramyl-L-alanyl-D-isogluatme (nor-MDP), N-acetylmuramyl-L-alanyl-D-isogluatminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-huydroxyphosphoryloxy)-ethylamine (MTP-PE), etc.

Dosage treatment with the VLP composition may be a single dose schedule or a multiple dose schedule. A multiple dose schedule is one in which a primary course of vaccination may be with 1-10 separate doses, followed by other doses given at subsequent time intervals, chosen to maintain and/or reinforce the immune response, for example at 1-4 months for a second dose, and if needed, a subsequent dose(s) after several months. The dosage regimen will also, at least in part, be determined by the potency of the modality, the vaccine delivery employed, the need of the subject and be dependent on the judgment of the practitioner.

If prevention of disease is desired (e.g., reduction of symptoms, recurrences or of disease progression), the antigen carrying VLPs are generally administered prior to primary infection with the pathogen of interest. If treatment is desired, e.g., the reduction of symptoms or recurrences, the VLP compositions are generally administered subsequent to primary infection.

2.2.2 USING THE SYNTHETIC EXPRESSION CASSETTES OF THE PRESENT INVENTION TO CREATE PACKAGING CELL LINES

A number of viral based systems have been developed for use as gene transfer vectors for mammalian host cells. For example, retroviruses (in particular,

lentiviral vectors) provide a convenient platform for gene delivery systems. A coding sequence of interest (for example, a sequence useful for gene therapy applications) can be inserted into a gene delivery vector and packaged in retroviral particles using techniques known in the art. Recombinant virus can then be isolated and delivered to cells of the subject either *in vivo* or *ex vivo*. A number of retroviral systems have been described, including, for example, the following: (U.S. Patent No. 5,219,740; Miller et al. (1989) *Biotechniques* 7:980; Miller, A.D. (1990) *Human Gene Therapy* 1:5; Scarpa et al. (1991) *Virology* 180:849; Burns et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:8033; Boris-Lawrie et al. (1993) *Cur. Opin. Genet. Develop.* 3:102; GB 2200651; EP 0415731; EP 0345242; WO 89/02468; WO 89/05349; WO 89/09271; WO 90/02806; WO 90/07936; WO 90/07936; WO 94/03622; WO 93/25698; WO 93/25234; WO 93/11230; WO 93/10218; WO 91/02805; in U.S. 5,219,740; U.S. 4,405,712; U.S. 4,861,719; U.S. 4,980,289 and U.S. 4,777,127; in U.S. Serial No. 07/800,921; and in Vile (1993) *Cancer Res* 53:3860-3864; Vile (1993) *Cancer Res* 53:962-967; Ram (1993) *Cancer Res* 53:83-88; Takamiya (1992) *J Neurosci Res* 33:493-503; Baba (1993) *J Neurosurg* 79:729-735; Mann (1983) *Cell* 33:153; Cane (1984) *Proc Natl Acad Sci USA* 81:6349; and Miller (1990) *Human Gene Therapy* 1.

Sequences useful for gene therapy applications include, but are not limited to, the following. Factor VIII cDNA, including derivatives and deletions thereof (International Publication Nos. WO 96/21035, WO 97/03193, WO 97/03194, WO 97/03195, and WO 97/03191). Factor IX cDNA (Kurachi et al. (1982) *Proc. Natl. Acad. Sci. USA* 79:6461-6464). Factor V cDNA can be obtained from pMT2-V (Jenny (1987) *Proc. Natl. Acad. Sci. USA* 84:4846, A.T.C.C. Deposit No. 40515). A full-length factor V

cDNA, or a B domain deletion or B domain substitution thereof, can be used. B domain deletions of factor V, include those reported by Marquette (1995) *Blood* 86:3026 and Kane (1990) *Biochemistry* 29:6762. Antithrombin III cDNA (Prochownik (1983) *J. Biol. Chem.* 258:8389, A.T.C.C. Deposit No. 57224/57225). Protein C encoding cDNA (Foster (1984) *Proc. Natl. Acad. Sci. USA* 81:4766; Beckmann (1985) *Nucleic Acids Res.* 13:5233). Prothrombin cDNA can be obtained by restriction enzyme digestion of a published vector (Degen (1983) *Biochemistry* 22:2087). The endothelial cell surface protein, thrombomodulin, is a necessary cofactor for the normal activation of protein C by thrombin. A soluble recombinant form has been described (Parkinson (1990) *J. Biol. Chem.* 265:12602; Jackman (1987) *Proc. Natl. Acad. Sci. USA* 84:6425; Shirai (1988) *J. Biochem.* 103:281; Wen (1987) *Biochemistry* 26:4350; Suzuki (1987) *EMBO J.* 6:1891, A.T.C.C. Deposit No. 61348, 61349).

Many genetic diseases caused by inheritance of defective genes result in the failure to produce normal gene products, for example, thalassemia, phenylketonuria, Lesch-Nyhan syndrome, severe combined immunodeficiency (SCID), hemophilia A and B, cystic fibrosis, Duchenne's Muscular Dystrophy, inherited emphysema and familial hypercholesterolemia (Mulligan et al. (1993) *Science* 260:926; Anderson et al. (1992) *Science* 256:808; Friedman et al. (1989) *Science* 244:1275). Although genetic diseases may result in the absence of a gene product, endocrine disorders, such as diabetes and hypopituitarism, are caused by the inability of the gene to produce adequate levels of the appropriate hormone insulin and human growth hormone respectively.

In one aspect, gene therapy employing the constructs and methods of the present invention involves the

introduction of normal recombinant genes into T cells so that new or missing proteins are produced by the T cells after introduction or reintroduction thereof into a patient. A number of genetic diseases have been selected
5 for treatment with gene therapy, including adenine deaminase deficiency, cystic fibrosis, α_1 -antitrypsin deficiency, Gaucher's syndrome, as well as non-genetic diseases.

In particular, Gaucher's syndrome is a genetic
10 disorder characterized by a deficiency of the enzyme glucocerebrosidase. This enzyme deficiency leads to the accumulation of glucocerebroside in the lysosomes of all cells in the body. For a review see *Science* 256:794 (1992) and Scriver et al., *The Metabolic Basis of*
15 *Inherited Disease*, 6th ed., vol. 2, page 1677). Thus, gene transfer vectors that express glucocerebrosidase can be constructed for use in the treatment of this disorder. Likewise, gene transfer vectors encoding lactase can be used in the treatment of hereditary lactose intolerance,
20 those expressing AD can be used for treatment of ADA deficiency, and gene transfer vectors encoding α_1 -antitrypsin can be used to treat α_1 -antitrypsin deficiency. See Ledley, F.D. (1987) *J. Pediatrics* 110:157-174, Verma, I. (Nov. 1987) *Scientific American*
25 pp. 68-84, and International Publication No. WO 95/27512 entitled "Gene Therapy Treatment for a Variety of Diseases and Disorders," for a description of gene therapy treatment of genetic diseases.

In still further embodiments of the invention,
30 nucleotide sequences which can be incorporated into a gene transfer vector include, but are not limited to, proteins associated with enzyme-deficiency disorders, such as the cystic fibrosis transmembrane regulator (see, for example, U.S. Patent No. 5,240,846 and Larrick et al.

(1991) *Gene Therapy Applications of Molecular Biology*, Elsevier, New York and adenosine deaminase (ADA) (see U.S. Patent No. 5,399,346); growth factors, or an agonist or antagonist of a growth factor (Bandara et al. (1992) 5 *DNA and Cell Biology*, 11:227); one or more tumor suppressor genes such as p53, Rb, or C-CAMI (Kleinerman et al. (1995) *Cancer Research* 55:2831); a molecule that modulates the immune system of an organism, such as a HLA molecule (Nabel et al. (1993) *Proc. Natl. Acad. Sci. USA* 10 90:11307); a ribozyme (Larsson et al. (1996) *Virology* 219:161); a peptide nucleic acid (Hirshman et al. (1996) *J. Invest. Med.* 44:347); an antisense molecule (Bordier et al. (1995) *Proc. Natl. Acad. Sci. USA* 92:9383) which can be used to down-regulate the expression or synthesis 15 of aberrant or foreign proteins, such as HIV proteins or a wide variety of oncogenes such as p53 (Hesketh, *The Oncogene Facts Book*, Academic Press, New York, (1995); a biopharmaceutical agent or antisense molecule used to treat HIV-infection, such as an inhibitor of p24 20 (Nakashima et al. (1994) *Nucleic Acids Res.* 22:5004); or reverse-transcriptase (see, Bordier, *supra*).

Other proteins of therapeutic interest can be expressed *in vivo* by gene transfer vectors using the methods of the invention. For instance sustained *in vivo* 25 expression of tissue factor inhibitory protein (TFPI) is useful for treatment of conditions including sepsis and DIC and in preventing reperfusion injury. (See International Publications Nos. WO 93/24143, WO 93/25230 and WO 96/06637). Nucleic acid sequences encoding 30 various forms of TFPI can be obtained, for example, as described in US Patent Nos. 4,966,852; 5,106,833; and 5,466,783, and incorporated into the gene transfer vectors described herein.

Erythropoietin (EPO) and leptin can also be expressed *in vivo* from genetically modified T cells according to the methods of the invention. For instance EPO is useful in gene therapy treatment of a variety of disorders including anemia (see International Publication No. WO 95/13376 entitled "Gene Therapy for Treatment of Anemia"). Sustained delivery of leptin by the methods of the invention is useful in treatment of obesity. See International Publication No. WO 96/05309 for a description of the leptin gene and the use thereof in the treatment of obesity.

A variety of other disorders can also be treated by the methods of the invention. For example, sustained *in vivo* systemic production of apolipoprotein E or apolipoprotein A from genetically modified T cells can be used for treatment of hyperlipidemia (see Breslow et al. (1994) *Biotechnology* 12:365). Sustained production of angiotensin receptor inhibitor (Goodfriend et al. (1996) *N. Engl. J. Med.* 334:1469) can be provided by the methods described herein. As yet an additional example, the long term *in vivo* systemic production of angiostatin is useful in the treatment of a variety of tumors. (See O'Reilly et al. (1996) *Nature Med.* 2:689).

In other embodiments, gene transfer vectors can be constructed to encode a cytokine or other immunomodulatory molecule. For example, nucleic acid sequences encoding native IL-2 and gamma-interferon can be obtained as described in US Patent Nos. 4,738,927 and 5,326,859, respectively, while useful muteins of these proteins can be obtained as described in U.S. Patent No. 4,853,332. Nucleic acid sequences encoding the short and long forms of mCSF can be obtained as described in US Patent Nos. 4,847,201 and 4,879,227, respectively. In particular aspects of the invention, retroviral vectors

expressing cytokine or immunomodulatory genes can be produced as described herein (for example, employing the packaging cell lines of the present invention) and in International Application No. PCT US 94/02951, entitled
5 "Compositions and Methods for Cancer Immunotherapy."

Examples of suitable immunomodulatory molecules for use herein include the following: IL-1 and IL-2 (Karupiah et al. (1990) *J. Immunology* 144:290-298, Weber et al. (1987) *J. Exp. Med.* 166:1716-1733, Gansbacher et al.
10 (1990) *J. Exp. Med.* 172:1217-1224, and U.S. Patent No. 4,738,927); IL-3 and IL-4 (Tepper et al. (1989) *Cell* 57:503-512, Golumbek et al. (1991) *Science* 254:713-716, and U.S. Patent No. 5,017,691); IL-5 and IL-6 (Brakenhof et al. (1987) *J. Immunol.* 139:4116-4121, and
15 International Publication No. WO 90/06370); IL-7 (U.S. Patent No. 4,965,195); IL-8, IL-9, IL-10, IL-11, IL-12, and IL-13 (*Cytokine Bulletin*, Summer 1994); IL-14 and IL-15; alpha interferon (Finter et al. (1991) *Drugs* 42:749-765, U.S. Patent Nos. 4,892,743 and 4,966,843,
20 International Publication No. WO 85/02862, Nagata et al. (1980) *Nature* 284:316-320, Familletti et al. (1981) *Methods in Enz.* 78:387-394, Twu et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:2046-2050, and Faktor et al. (1990) *Oncogene* 5:867-872); beta-interferon (Seif et al. (1991)
25 *J. Virol.* 65:664-671); gamma-interferons (Radford et al. (1991) *The American Society of Hepatology* 20082015, Watanabe et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:9456-9460, Gansbacher et al. (1990) *Cancer Research* 50:7820-7825, Maio et al. (1989) *Can. Immunol.*
30 *Immunother.* 30:34-42, and U.S. Patent Nos. 4,762,791 and 4,727,138); G-CSF (U.S. Patent Nos. 4,999,291 and 4,810,643); GM-CSF (International Publication No. WO 85/04188); tumor necrosis factors (TNFs) (Jayaraman et al. (1990) *J. Immunology* 144:942-951); CD3 (Krissanen et

al. (1987) *Immunogenetics* 26:258-266); ICAM-1 (Altman et al. (1989) *Nature* 338:512-514, Simmons et al. (1988) *Nature* 331:624-627); ICAM-2, LFA-1, LFA-3 (Wallner et al. (1987) *J. Exp. Med.* 166:923-932); MHC class I molecules,
5 MHC class II molecules, B7.1-.3, β_2 -microglobulin (Parnes et al. (1981) *Proc. Natl. Acad. Sci. USA* 78:2253-2257); chaperones such as calnexin; and MHC-linked transporter proteins or analogs thereof (Powis et al. (1991) *Nature* 354:528-531). Immunomodulatory factors may also be
10 agonists, antagonists, or ligands for these molecules. For example, soluble forms of receptors can often behave as antagonists for these types of factors, as can mutated forms of the factors themselves.

Nucleic acid molecules that encode the above-
15 described substances, as well as other nucleic acid molecules that are advantageous for use within the present invention, may be readily obtained from a variety of sources, including, for example, depositories such as the American Type Culture Collection, or from commercial
20 sources such as British Bio-Technology Limited (Cowley, Oxford England). Representative examples include BBG 12 (containing the GM-CSF gene coding for the mature protein of 127 amino acids), BBG 6 (which contains sequences encoding gamma interferon), A.T.C.C. Deposit No. 39656
25 (which contains sequences encoding TNF), A.T.C.C. Deposit No. 20663 (which contains sequences encoding alpha-interferon), A.T.C.C. Deposit Nos. 31902, 31902 and 39517 (which contain sequences encoding beta-interferon), A.T.C.C. Deposit No. 67024 (which contains a sequence
30 which encodes Interleukin-1b), A.T.C.C. Deposit Nos. 39405, 39452, 39516, 39626 and 39673 (which contain sequences encoding Interleukin-2), A.T.C.C. Deposit Nos. 59399, 59398, and 67326 (which contain sequences encoding Interleukin-3), A.T.C.C. Deposit No. 57592 (which

contains sequences encoding Interleukin-4), A.T.C.C. Deposit Nos. 59394 and 59395 (which contain sequences encoding Interleukin-5), and A.T.C.C. Deposit No. 67153 (which contains sequences encoding Interleukin-6).

5 Plasmids containing cytokine genes or immunomodulatory genes (International Publication Nos. WO 94/02951 and WO 96/21015) can be digested with appropriate restriction enzymes, and DNA fragments containing the particular gene of interest can be inserted into a gene
10 transfer vector using standard molecular biology techniques. (See, e.g., Sambrook et al., *supra.*, or Ausubel et al. (eds) *Current Protocols in Molecular Biology*, Greene Publishing and Wiley-Interscience).

Exemplary hormones, growth factors and other
15 proteins which are useful for long term expression are described, for example, in European Publication No. 0437478B1, entitled "Cyclodextrin-Peptide Complexes." Nucleic acid sequences encoding a variety of hormones can be used, including those encoding human growth hormone,
20 insulin, calcitonin, prolactin, follicle stimulating hormone (FSH), luteinizing hormone (LH), human chorionic gonadotropin (HCG), and thyroid stimulating hormone (TSH). A variety of different forms of IGF-1 and IGF-2 growth factor polypeptides are also well known the art
25 and can be incorporated into gene transfer vectors for long term expression *in vivo*. See, e.g., European Patent No. 0123228B1, published for grant September 19, 1993, entitled "Hybrid DNA Synthesis of Mature Insulin-like Growth Factors." As an additional example, the long term
30 *in vivo* expression of different forms of fibroblast growth factor can also be effected employing the compositions and methods of invention. See, e.g., U.S. Patent Nos. 5,464,774, 5,155,214, and 4,994,559 for a description of different fibroblast growth factors.

Polynucleotide sequences coding for the above-described molecules can be obtained using recombinant methods, such as by screening cDNA and genomic libraries from cells expressing the gene, or by deriving the gene
5 from a vector known to include the same. For example, plasmids which contain sequences that encode altered cellular products may be obtained from a depository such as the A.T.C.C., or from commercial sources. Plasmids containing the nucleotide sequences of interest can be
10 digested with appropriate restriction enzymes, and DNA fragments containing the nucleotide sequences can be inserted into a gene transfer vector using standard molecular biology techniques.

Alternatively, cDNA sequences for use with the
15 present invention may be obtained from cells which express or contain the sequences, using standard techniques, such as phenol extraction and PCR of cDNA or genomic DNA. See, e.g., Sambrook et al., *supra*, for a description of techniques used to obtain and isolate DNA.
20 Briefly, mRNA from a cell which expresses the gene of interest can be reverse transcribed with reverse transcriptase using oligo-dT or random primers. The single stranded cDNA may then be amplified by PCR (see U.S. Patent Nos. 4,683,202, 4,683,195 and 4,800,159, see
25 also *PCR Technology: Principles and Applications for DNA Amplification*, Erlich (ed.), Stockton Press, 1989)) using oligonucleotide primers complementary to sequences on either side of desired sequences.

The nucleotide sequence of interest can also be
30 produced synthetically, rather than cloned, using a DNA synthesizer (e.g., an Applied Biosystems Model 392 DNA Synthesizer, available from ABI, Foster City, California). The nucleotide sequence can be designed with the appropriate codons for the expression product

desired. The complete sequence is assembled from overlapping oligonucleotides prepared by standard methods and assembled into a complete coding sequence. See, e.g., Edge (1981) *Nature* 292:756; Nambair et al. (1984) *Science* 223:1299; Jay et al. (1984) *J. Biol. Chem.* 259:6311.

The synthetic expression cassettes of the present invention can be employed in the construction of packaging cell lines for use with retroviral vectors.

One type of retrovirus, the murine leukemia virus, or "MLV", has been widely utilized for gene therapy applications (see generally Mann et al. (*Cell* 33:153, 1993), Cane and Mulligan (*Proc. Nat'l. Acad. Sci. USA* 81:6349, 1984), and Miller et al., *Human Gene Therapy* 1:5-14, 1990).

Lentiviral vectors typically, comprise a 5' lentiviral LTR, a tRNA binding site, a packaging signal, a promoter operably linked to one or more genes of interest, an origin of second strand DNA synthesis and a 3' lentiviral LTR, wherein the lentiviral vector contains a nuclear transport element. The nuclear transport element may be located either upstream (5') or downstream (3') of a coding sequence of interest. Within certain embodiments, the nuclear transport element is not RRE. Within one embodiment the packaging signal is an extended packaging signal. Within other embodiments the promoter is a tissue specific promoter, or, alternatively, a promoter such as CMV. Within other embodiments, the lentiviral vector further comprises an internal ribosome entry site.

A wide variety of lentiviruses may be utilized within the context of the present invention, including for example, lentiviruses selected from the group consisting of HIV, HIV-1, HIV-2, FIV and SIV.

In one embodiment of the present invention synthetic Env and/or Gag-polymerase expression cassettes are provided comprising a promoter and a sequence encoding synthetic Gag-polymerase (SEQ ID NO:6) and at least one
5 of vpr, vpu, nef or vif, wherein the promoter is operably linked to Gag-polymerase and vpr, vpu, nef or vif.

Within yet another aspect of the invention, host cells (e.g., packaging cell lines) are provided which contain any of the expression cassettes described herein.
10 For example, within one aspect packaging cell line are provided comprising an expression cassette that comprises a sequence encoding synthetic Env and/or Gag-polymerase, and a nuclear transport element, wherein the promoter is operably linked to the sequence encoding Env and/or Gag-
15 polymerase. Packaging cell lines may further comprise a promoter and a sequence encoding tat, rev, or an envelope, wherein the promoter is operably linked to the sequence encoding tat, rev, or, the envelope. The packaging cell line may further comprise a sequence
20 encoding any one or more of nef, vif, vpu or vpr.

In one embodiment, the expression cassette (carrying, for example, the synthetic Env, synthetic tat and/or synthetic Gag-polymerase) is stably integrated. The packaging cell line, upon introduction of a
25 lentiviral vector, typically produces viral particles. The promoter regulating expression of the synthetic expression cassette may be inducible. Typically, the packaging cell line, upon introduction of a lentiviral vector, produces viral particles that are essentially
30 free of replication competent virus.

Packaging cell lines are provided comprising an expression cassette which directs the expression of a synthetic Env (or Gag-polymerase) gene, an expression cassette which directs the expression of a Gag (or Env)

gene optimized for expression (e.g., Andre, S., et al., *Journal of Virology* 72(2):1497-1503, 1998; Haas, J., et al., *Current Biology* 6(3):315-324, 1996). A lentiviral vector is introduced into the packaging cell line to
5 produce a vector particle producing cell line.

As noted above, lentiviral vectors can be designed to carry or express a selected gene(s) or sequences of interest. Lentiviral vectors may be readily constructed from a wide variety of lentiviruses (see RNA Tumor
10 Viruses, Second Edition, Cold Spring Harbor Laboratory, 1985). Representative examples of lentiviruses included HIV, HIV-1, HIV-2, FIV and SIV. Such lentiviruses may either be obtained from patient isolates, or, more preferably, from depositories or collections such as the
15 American Type Culture Collection, or isolated from known sources using available techniques.

Portions of the lentiviral gene delivery vectors (or vehicles) may be derived from different viruses. For example, in a given recombinant lentiviral vector, LTRs
20 may be derived from an HIV, a packaging signal from SIV, and an origin of second strand synthesis from HrV-2. Lentiviral vector constructs may comprise a 5' lentiviral LTR, a tRNA binding site, a packaging signal, one or more heterologous sequences, an origin of second strand DNA
25 synthesis and a 3' LTR, wherein said lentiviral vector contains a nuclear transport element that is not RRE.

Briefly, Long Terminal Repeats ("LTRs") are subdivided into three elements, designated U5, R and U3. These elements contain a variety of signals which are
30 responsible for the biological activity of a retrovirus, including for example, promoter and enhancer elements which are located within U3. LTRs may be readily identified in the provirus (integrated DNA form) due to their precise duplication at either end of the genome.

As utilized herein, a 5' LTR should be understood to include a 5' promoter element and sufficient LTR sequence to allow reverse transcription and integration of the DNA form of the vector. The 3' LTR should be understood to include a polyadenylation signal, and sufficient LTR sequence to allow reverse transcription and integration of the DNA form of the vector.

The tRNA binding site and origin of second strand DNA synthesis are also important for a retrovirus to be biologically active, and may be readily identified by one of skill in the art. For example, retroviral tRNA binds to a tRNA binding site by Watson-Crick base pairing, and is carried with the retrovirus genome into a viral particle. The tRNA is then utilized as a primer for DNA synthesis by reverse transcriptase. The tRNA binding site may be readily identified based upon its location just downstream from the 5'LTR. Similarly, the origin of second strand DNA synthesis is, as its name implies, important for the second strand DNA synthesis of a retrovirus. This region, which is also referred to as the poly-purine tract, is located just upstream of the 3'LTR.

In addition to a 5' and 3' LTR, tRNA binding site, and origin of second strand DNA synthesis, recombinant retroviral vector constructs may also comprise a packaging signal, as well as one or more genes or coding sequences of interest. In addition, the lentiviral vectors have a nuclear transport element which, in preferred embodiments is not RRE. Representative examples of suitable nuclear transport elements include the element in Rous sarcoma virus (Ogert, et al., *J ViroL* 70, 3834-3843, 1996), the element in Rous sarcoma virus (Liu & Mertz, *Genes & Dev.*, 9, 1766-1789, 1995) and the element in the genome of simian retrovirus type I

(Zolotukhin, et al., *J Virol.* 68, 7944-7952, 1994).

Other potential elements include the elements in the histone gene (Kedes, *Annu. Rev. Biochem.* 48, 837-870, 1970), the α -interferon gene (Nagata et al., *Nature* 287, 401-408, 1980), the β -adrenergic receptor gene (Koilkka, et al., *Nature* 329, 75-79, 1987), and the c-Jun gene (Hattorie, et al., *Proc. Natl. Acad. Sci. USA* 85, 9148-9152, 1988).

Recombinant lentiviral vector constructs typically lack both *Gag-polymerase* and *env* coding sequences. Recombinant lentiviral vector typically contain less than 20, preferably 15, more preferably 10, and most preferably 8 consecutive nucleotides found in *Gag-polymerase* or *env* genes. One advantage of the present invention is that the synthetic *Gag-polymerase* expression cassettes, which can be used to construct packaging cell lines for the recombinant retroviral vector constructs, have little homology to wild-type *Gag-polymerase* sequences and thus considerably reduce or eliminate the possibility of homologous recombination between the synthetic and wild-type sequences.

Lentiviral vectors may also include tissue-specific promoters to drive expression of one or more genes or sequences of interest. For example, lentiviral vector particles of the invention can contain a liver specific promoter to maximize the potential for liver specific expression of the exogenous DNA sequence contained in the vectors. Preferred liver specific promoters include the hepatitis B X-gene promoter and the hepatitis B core protein promoter. These liver specific promoters are preferably employed with their respective enhancers. The enhancer element can be linked at either the 5' or the 3' end of the nucleic acid encoding the sequences of interest. The hepatitis B X gene promoter and its

enhancer can be obtained from the viral genome as a 332 base pair *EcoRV*-*NcoI* DNA fragment employing the methods described in Twu, et al., *J Virol.* 61:3448-3453, 1987. The hepatitis B core protein promoter can be obtained
5 from the viral genome as a 584 base pair *BamHI*-*BglIII* DNA fragment employing the methods described in Gerlach, et al., *Virol* 189:59-66, 1992. It may be necessary to remove the negative regulatory sequence in the *BamHI*-*BglIII* fragment prior to inserting it. Other liver
10 specific promoters include the AFP (alpha fetal protein) gene promoter and the albumin gene promoter, as disclosed in EP Patent Publication 0 415 731, the -1 antitrypsin gene promoter, as disclosed in Rettenger, et al., *Proc. Natl. Acad. Sci.* 91:1460-1464, 1994, the fibrinogen
15 gene promoter, the APO-A1 (Apolipoprotein A1) gene promoter, and the promoter genes for liver transference enzymes such as, for example, SGOT, SGPT and glutamyle transferase. See also PCT Patent Publications WO 90/07936 and WO 91/02805 for a description of the use of
20 liver specific promoters in lentiviral vector particles.

Lentiviral vector constructs may be generated such that more than one gene of interest is expressed. This may be accomplished through the use of di- or oligo-cistronic cassettes (e.g., where the coding regions are
25 separated by 80 nucleotides or less, see generally Levin et al., *Gene* 108:167-174, 1991), or through the use of Internal Ribosome Entry Sites ("IRES").

Packaging cell lines suitable for use with the above described recombinant retroviral vector constructs may be
30 readily prepared given the disclosure provided herein. Briefly, the parent cell line from which the packaging cell line is derived can be selected from a variety of

mammalian cell lines, including for example, 293, RD, COS-7, CHO, BHK, VERO, HT1080, and myeloma cells.

After selection of a suitable host cell for the generation of a packaging cell line, one or more
5 expression cassettes are introduced into the cell line in order to complement or supply in *trans* components of the vector which have been deleted.

Representative examples of suitable expression cassettes have been described herein and include
10 synthetic Env, tat, Gag, synthetic Gag-protease, synthetic Gag-reverse transcriptase and synthetic Gag-polymerase expression cassettes, which comprise a promoter and a sequence encoding, e.g., Env, tat, or Gag-polymerase and at least one of vpr, vpu, nef or vif,
15 wherein the promoter is operably linked to Env, tat or Gag-polymerase and vpr, vpu, nef or vif. As described above, optimized Env, Gag and/or tat coding sequences may also be utilized in various combinations in the generation of packaging cell lines.

20 Utilizing the above-described expression cassettes, a wide variety of packaging cell lines can be generated. For example, within one aspect packaging cell line are provided comprising an expression cassette that comprises a sequence encoding synthetic HIV (e.g., Gag, Env, tat, Gag-polymerase, Gag-reverse transcriptase or Gag-
25 protease) polypeptide, and a nuclear transport element, wherein the promoter is operably linked to the sequence encoding the HIV polypeptide. Within other aspects, packaging cell lines are provided comprising a promoter
30 and a sequence encoding Gag, tat, rev, or an envelope (e.g., HIV env), wherein the promoter is operably linked to the sequence encoding Gag, tat, rev, or, the envelope. Within further embodiments, the packaging cell line may comprise a sequence encoding any one or more of nef, vif,

vpu or vpr. For example, the packaging cell line may contain only nef, vif, vpu, or vpr alone, nef and vif, nef and vpu, nef and vpr, vif and vpu, vif and vpr, vpu and vpr, nef vif and vpu, nef vif and vpr, nef vpu and vpr, vvir vpu and vpr, or, all four of nef vif vpu and vpr.

In one embodiment, the expression cassette is stably integrated. Within another embodiment, the packaging cell line, upon introduction of a lentiviral vector, produces particles. Within further embodiments the promoter is inducible. Within certain preferred embodiments of the invention, the packaging cell line, upon introduction of a lentiviral vector, produces particles that are free of replication competent virus.

The synthetic cassettes containing optimized coding sequences are transfected into a selected cell line. Transfected cells are selected that (i) carry, typically, integrated, stable copies of the Gag, Pol, and Env coding sequences, and (ii) are expressing acceptable levels of these polypeptides (expression can be evaluated by methods known in the prior art, e.g., see Examples 1-4). The ability of the cell line to produce VLPs may also be verified (Examples 6, 7 and 15).

A sequence of interest is constructed into a suitable viral vector as discussed above. This defective virus is then transfected into the packaging cell line. The packaging cell line provides the viral functions necessary for producing virus-like particles into which the defective viral genome, containing the sequence of interest, are packaged. These VLPs are then isolated and can be used, for example, in gene delivery or gene therapy.

Further, such packaging cell lines can also be used to produce VLPs alone, which can, for example, be used as

adjuvants for administration with other antigens or in vaccine compositions. Also, co-expression of a selected sequence of interest encoding a polypeptide (for example, an antigen) in the packaging cell line can also result in
5 the entrapment and/or association of the selected polypeptide in/with the VLPs.

2.3 DNA IMMUNIZATION AND GENE DELIVERY

A variety of polypeptide antigens can be used in the
10 practice of the present invention. Polypeptide antigens can be included in DNA immunization constructs containing, for example, any of the synthetic expression cassettes described herein fused in-frame to a coding sequence for the polypeptide antigen, where expression of
15 the construct results in VLPs presenting the antigen of interest. Antigens can be derived from a wide variety of viruses, bacteria, fungi, plants, protozoans and other parasites. For example, the present invention will find use for stimulating an immune response against a wide
20 variety of proteins from the herpesvirus family, including proteins derived from herpes simplex virus (HSV) types 1 and 2, such as HSV-1 and HSV-2 gB, gD, gH, VP16 and VP22; antigens derived from varicella zoster virus (VZV), Epstein-Barr virus (EBV) and cytomegalovirus
25 (CMV) including CMV gB and gH; and antigens derived from other human herpesviruses such as HHV6 and HHV7. (See, e.g. Chee et al., *Cytomegaloviruses* (J.K. McDougall, ed., Springer-Verlag 1990) pp. 125-169, for a review of the protein coding content of cytomegalovirus; McGeoch et al., *J. Gen. Virol.* (1988) 69:1531-1574, for a discussion
30 of the various HSV-1 encoded proteins; U.S. Patent No. 5,171,568 for a discussion of HSV-1 and HSV-2 gB and gD proteins and the genes encoding therefore; Baer et al., *Nature* (1984) 310:207-211, for the identification of

protein coding sequences in an EBV genome; and Davison and Scott, *J. Gen. Virol.* (1986) 67:1759-1816, for a review of VZV.)

5 Additionally, immune responses to antigens from the hepatitis family of viruses, including hepatitis A virus (HAV), hepatitis B virus (HBV), hepatitis C virus (HCV), the delta hepatitis virus (HDV), hepatitis E virus (HEV), and hepatitis G virus, can also be stimulated using the constructs of the present invention. By way of example,
10 the HCV genome encodes several viral proteins, including E1 (also known as E) and E2 (also known as E2/NSI), which will find use with the present invention (see, Houghton et al. *Hepatology* (1991) 14:381-388, for a discussion of HCV proteins, including E1 and E2). The δ -antigen from
15 HDV can also be used (see, e.g., U.S. Patent No. 5,389,528, for a description of the δ -antigen).

Similarly, influenza virus is another example of a virus for which the present invention will be particularly useful. Specifically, the envelope
20 glycoproteins HA and NA of influenza A are of particular interest for generating an immune response. Numerous HA subtypes of influenza A have been identified (Kawaoka et al., *Virology* (1990) 179:759-767; Webster et al. "Antigenic variation among type A influenza viruses," p.
25 127-168. In: P. Palese and D.W. Kingsbury (ed.), *Genetics of influenza viruses*. Springer-Verlag, New York).

Other antigens of particular interest to be used in the practice of the present invention include antigens and polypeptides derived therefrom from human
30 papillomavirus (HPV), such as one or more of the various early proteins including E6 and E7; tick-borne encephalitis viruses; and HIV-1 (also known as HTLV-III, LAV, ARV, etc.), including, but not limited to, antigens such as gp120, gp41, gp160, Gag and pol from a variety of

isolates including, but not limited to, HIV_{IIb}, HIV_{SF2}, HIV-1_{SF162}, HIV-1_{SF170}, HIV_{LAV}, HIV_{LA1}, HIV_{MN}, HIV-1_{CM235}, HIV-1_{US4}, other HIV-1 strains from diverse subtypes (e.g., subtypes, A through G, and O), HIV-2 strains and diverse subtypes (e.g., HIV-2_{UC1} and HIV-2_{UC2}). See, e.g., Myers, et al., Los Alamos Database, Los Alamos National Laboratory, Los Alamos, New Mexico; Myers, et al., *Human Retroviruses and Aids*, 1990, Los Alamos, New Mexico: Los Alamos National Laboratory.

Proteins derived from other viruses will also find use in the claimed methods, such as without limitation, proteins from members of the families Picornaviridae (e.g., polioviruses, etc.); Caliciviridae; Togaviridae (e.g., rubella virus, dengue virus, etc.); Flaviviridae; Coronaviridae; Reoviridae; Birnaviridae; Rhabdoviridae (e.g., rabies virus, etc.); Filoviridae; Paramyxoviridae (e.g., mumps virus, measles virus, respiratory syncytial virus, etc.); Orthomyxoviridae (e.g., influenza virus types A, B and C, etc.); Bunyaviridae; Arenaviridae; Retroviridae, e.g., HTLV-I; HTLV-II; HIV-1; HIV-2; simian immunodeficiency virus (SIV) among others. See, e.g. *Virology*, 3rd Edition (W.K. Joklik ed. 1988); *Fundamental Virology*, 2nd Edition (B.N. Fields and D.M. Knipe, eds. 1991; *Virology*, 3rd Edition (Fields, BN, DM Knipe, PM Howley, Editors, 1996, Lippincott-Raven, Philadelphia, PA) for a description of these and other viruses.

Particularly preferred bacterial antigens are derived from organisms that cause diphtheria, tetanus, pertussis, meningitis, and other pathogenic states, including, without limitation, antigens derived from *Corynebacterium diphtheriae*, *Clostridium tetani*, *Bordetella pertussis*, *Neisseria meningitidis*, including serotypes *Meningococcus* A, B, C, Y and WI35 (MenA, B, C, Y and WI35), *Haemophilus influenza* type B (Hib), and

Helicobacter pylori. Examples of parasitic antigens include those derived from organisms causing malaria, tuberculosis, and Lyme disease.

Furthermore, the methods described herein provide
5 means for treating a variety of malignant cancers. For example, the system of the present invention can be used to enhance both humoral and cell-mediated immune responses to particular proteins specific to a cancer in question, such as an activated oncogene, a fetal antigen,
10 or an activation marker. Such tumor antigens include any of the various MAGEs (melanoma associated antigen E), including MAGE 1, 2, 3, 4, etc. (Boon, T. *Scientific American* (March 1993):82-89); any of the various tyrosinases; MART 1 (melanoma antigen recognized by T
15 cells), mutant ras; mutant p53; p97 melanoma antigen; CEA (carcinoembryonic antigen), among others.

DNA immunization using synthetic expression cassettes of the present invention has been demonstrated to be efficacious (Examples 8 and 10-12). Animals were
20 immunized with both the synthetic expression cassette and the wild type expression cassette. The results of the immunizations with plasmid-DNAs showed that the synthetic expression cassettes provide a clear improvement of immunogenicity relative to the native expression
25 cassettes. Also, the second boost immunization induced a secondary immune response, for example after two to eight weeks. Further, the results of CTL assays showed increased potency of synthetic expression cassettes for induction of cytotoxic T-lymphocyte (CTL) responses by
30 DNA immunization.

It is readily apparent that the subject invention can be used to mount an immune response to a wide variety of antigens and hence to treat or prevent a large number of diseases.

2.3.1 DELIVERY OF THE SYNTHETIC EXPRESSION CASSETTES OF THE
PRESENT INVENTION

Polynucleotide sequences coding for the above-described molecules can be obtained using recombinant
5 methods, such as by screening cDNA and genomic libraries from cells expressing the gene, or by deriving the gene from a vector known to include the same. The sequences can be analyzed by conventional sequencing techniques. Furthermore, the desired gene can be isolated directly
10 from cells and tissues containing the same, using standard techniques, such as phenol extraction and PCR of cDNA or genomic DNA. See, e.g., Sambrook et al., *supra*, for a description of techniques used to obtain, isolate and sequence DNA. Once the sequence is known, the gene
15 of interest can also be produced synthetically, rather than cloned. The nucleotide sequence can be designed with the appropriate codons for the particular amino acid sequence desired. In general, one will select preferred codons for the intended host in which the sequence will
20 be expressed. The complete sequence is assembled from overlapping oligonucleotides prepared by standard methods and assembled into a complete coding sequence. See, e.g., Edge, *Nature* (1981) 292:756; Nambair et al., *Science* (1984) 223:1299; Jay et al., *J. Biol. Chem.* (1984) 259:6311; Stemmer, W.P.C., (1995) *Gene* 164:49-53.

Next, the gene sequence encoding the desired antigen can be inserted into a vector containing a synthetic expression cassette of the present invention (e.g., see
30 Example 1 for construction of various exemplary synthetic expression cassette). The antigen is inserted into the synthetic coding sequence such that when the combined sequence is expressed it results in the production of VLPs comprising the polypeptide and/or the antigen of

interest. Insertions can be made within the Gag coding sequence or at either end of the coding sequence (5', amino terminus of the expressed polypeptide; or 3', carboxy terminus of the expressed polypeptide -- e.g.,
5 see Example 1) (Wagner, R., et al., *Arch Virol.* 127:117-137, 1992; Wagner, R., et al., *Virology* 200:162-175, 1994; Wu, X., et al., *J. Virol.* 69(6):3389-3398, 1995; Wang, C-T., et al., *Virology* 200:524-534, 1994; Chazal, N., et al., *Virology* 68(1):111-122, 1994; Griffiths,
10 J.C., et al., *J. Virol.* 67(6):3191-3198, 1993; Reicin, A.S., et al., *J. Virol.* 69(2):642-650, 1995).

Up to 50% of the coding sequences of p55Gag can be deleted without affecting the assembly to virus-like particles and expression efficiency (Borsetti, A., et al.,
15 *J. Virol.* 72(11):9313-9317, 1998; Gamier, L., et al., *J Virol* 72(6):4667-4677, 1998; Zhang, Y., et al., *J Virol* 72(3):1782-1789, 1998; Wang, C., et al., *J Virol* 72(10):7950-7959, 1998). In one embodiment of the present invention, immunogenicity of the high level expressing
20 synthetic p55GagMod and p55GagProtMod expression cassettes can be increased by the insertion of different structural or non-structural HIV antigens, multiepitope cassettes, or cytokine sequences into deleted, mutated or truncated regions of p55GagMod sequence. In another
25 embodiment of the present invention, immunogenicity of the high level expressing synthetic Env expression cassettes can be increased by the insertion of different structural or non-structural HIV antigens, multiepitope cassettes, or cytokine sequences into deleted regions of
30 gp120Mod, gp140Mod or gp160Mod sequences. Such deletions may be generated following the teachings of the present invention and information available to one of ordinary skill in the art. One possible advantage of this approach, relative to using full-length modified Env

sequences fused to heterologous polypeptides, can be higher expression/secretion efficiency and/or higher immunogenicity of the expression product. Such deletions may be generated following the teachings of the present invention and information available to one of ordinary skill in the art. One possible advantage of this approach, relative to using full-length Env, Gag or Tat sequences fused to heterologous polypeptides, can be higher expression/secretion efficiency and/or immunogenicity of the expression product.

When sequences are added to the amino terminal end of Gag (for example, when using the synthetic p55GagMod expression cassette of the present invention), the polynucleotide can contain coding sequences at the 5' end that encode a signal for addition of a myristic moiety to the Gag-containing polypeptide (e.g., sequences that encode Met-Gly).

The ability of Gag-containing polypeptide constructs to form VLPs can be empirically determined following the teachings of the present specification.

HIV polypeptide/antigen synthetic expression cassettes include control elements operably linked to the coding sequence, which allow for the expression of the gene *in vivo* in the subject species. For example, typical promoters for mammalian cell expression include the SV40 early promoter, a CMV promoter such as the CMV immediate early promoter, the mouse mammary tumor virus LTR promoter, the adenovirus major late promoter (Ad MLP), and the herpes simplex virus promoter, among others. Other nonviral promoters, such as a promoter derived from the murine metallothionein gene, will also find use for mammalian expression. Typically, transcription termination and polyadenylation sequences will also be present, located 3' to the translation stop

codon. Preferably, a sequence for optimization of initiation of translation, located 5' to the coding sequence, is also present. Examples of transcription terminator/polyadenylation signals include those derived from SV40, as described in Sambrook et al., *supra*, as well as a bovine growth hormone terminator sequence.

Enhancer elements may also be used herein to increase expression levels of the mammalian constructs. Examples include the SV40 early gene enhancer, as described in Dijkema et al., *EMBO J.* (1985) 4:761, the enhancer/promoter derived from the long terminal repeat (LTR) of the Rous Sarcoma Virus, as described in Gorman et al., *Proc. Natl. Acad. Sci. USA* (1982b) 79:6777 and elements derived from human CMV, as described in Boshart et al., *Cell* (1985) 41:521, such as elements included in the CMV intron A sequence.

Furthermore, plasmids can be constructed which include a chimeric antigen-coding gene sequences, encoding, e.g., multiple antigens/epitopes of interest, for example derived from a single or from more than one viral isolate.

Typically the antigen coding sequences precede or follow the synthetic coding sequences and the chimeric transcription unit will have a single open reading frame encoding both the antigen of interest and the synthetic Gag coding sequences. Alternatively, multi-cistronic cassettes (e.g., bi-cistronic cassettes) can be constructed allowing expression of multiple antigens from a single mRNA using the EMCV IRES, or the like. Lastly, antigens can be encoded on separate transcripts from independent promoters on a single plasmid or other vector.

Once complete, the constructs are used for nucleic acid immunization or the like using standard gene

delivery protocols. Methods for gene delivery are known in the art. See, e.g., U.S. Patent Nos. 5,399,346, 5,580,859, 5,589,466. Genes can be delivered either directly to the vertebrate subject or, alternatively,
5 delivered ex vivo, to cells derived from the subject and the cells reimplanted in the subject.

A number of viral based systems have been developed for gene transfer into mammalian cells. For example, retroviruses provide a convenient platform for gene
10 delivery systems. Selected sequences can be inserted into a vector and packaged in retroviral particles using techniques known in the art. The recombinant virus can then be isolated and delivered to cells of the subject either in vivo or ex vivo. A number of retroviral
15 systems have been described (U.S. Patent No. 5,219,740; Miller and Rosman, *BioTechniques* (1989) 7:980-990; Miller, A.D., *Human Gene Therapy* (1990) 1:5-14; Scarpa et al., *Virology* (1991) 180:849-852; Burns et al., *Proc. Natl. Acad. Sci. USA* (1993) 90:8033-8037; and Boris-
20 Lawrie and Temin, *Cur. Opin. Genet. Develop.* (1993) 3:102-109.

A number of adenovirus vectors have also been described. Unlike retroviruses which integrate into the host genome, adenoviruses persist extrachromosomally thus
25 minimizing the risks associated with insertional mutagenesis (Haj-Ahmad and Graham, *J. Virol.* (1986) 57:267-274; Bett et al., *J. Virol.* (1993) 67:5911-5921; Mittereder et al., *Human Gene Therapy* (1994) 5:717-729; Seth et al., *J. Virol.* (1994) 68:933-940; Barr et al.,
30 *Gene Therapy* (1994) 1:51-58; Berkner, K.L. *BioTechniques* (1988) 6:616-629; and Rich et al., *Human Gene Therapy* (1993) 4:461-476).

Additionally, various adeno-associated virus (AAV) vector systems have been developed for gene delivery.

AAV vectors can be readily constructed using techniques well known in the art. See, e.g., U.S. Patent Nos. 5,173,414 and 5,139,941; International Publication Nos. WO 92/01070 (published 23 January 1992) and WO 93/03769 (published 4 March 1993); Lebkowski et al., *Molec. Cell. Biol.* (1988) 8:3988-3996; Vincent et al., *Vaccines* 90 (1990) (Cold Spring Harbor Laboratory Press); Carter, B.J. *Current Opinion in Biotechnology* (1992) 3:533-539; Muzyczka, N. *Current Topics in Microbiol. and Immunol.* (1992) 158:97-129; Kotin, R.M. *Human Gene Therapy* (1994) 5:793-801; Shelling and Smith, *Gene Therapy* (1994) 1:165-169; and Zhou et al., *J. Exp. Med.* (1994) 179:1867-1875.

Another vector system useful for delivering the polynucleotides of the present invention is the enterically administered recombinant poxvirus vaccines described by Small, Jr., P.A., et al. (U.S. Patent No. 5,676,950, issued October 14, 1997).

Additional viral vectors which will find use for delivering the nucleic acid molecules encoding the antigens of interest include those derived from the pox family of viruses, including vaccinia virus and avian poxvirus. By way of example, vaccinia virus recombinants expressing the genes can be constructed as follows. The DNA encoding the particular synthetic Gag/antigen coding sequence is first inserted into an appropriate vector so that it is adjacent to a vaccinia promoter and flanking vaccinia DNA sequences, such as the sequence encoding thymidine kinase (TK). This vector is then used to transfect cells which are simultaneously infected with vaccinia. Homologous recombination serves to insert the vaccinia promoter plus the gene encoding the coding sequences of interest into the viral genome. The resulting TK recombinant can be selected by culturing the

cells in the presence of 5-bromodeoxyuridine and picking viral plaques resistant thereto.

Alternatively, avipoxviruses, such as the fowlpox and canarypox viruses, can also be used to deliver the genes. Recombinant avipox viruses, expressing immunogens from mammalian pathogens, are known to confer protective immunity when administered to non-avian species. The use of an avipox vector is particularly desirable in human and other mammalian species since members of the avipox genus can only productively replicate in susceptible avian species and therefore are not infective in mammalian cells. Methods for producing recombinant avipoxviruses are known in the art and employ genetic recombination, as described above with respect to the production of vaccinia viruses. See, e.g., WO 91/12882; WO 89/03429; and WO 92/03545.

Molecular conjugate vectors, such as the adenovirus chimeric vectors described in Michael et al., *J. Biol. Chem.* (1993) 268:6866-6869 and Wagner et al., *Proc. Natl. Acad. Sci. USA* (1992) 89:6099-6103, can also be used for gene delivery.

Members of the Alphavirus genus, such as, but not limited to, vectors derived from the Sindbis, Semliki Forest, and Venezuelan Equine Encephalitis viruses, will also find use as viral vectors for delivering the polynucleotides of the present invention (for example, a synthetic Gag- or Env-polypeptide encoding expression cassette as described in Example 14 below). For a description of Sindbis-virus derived vectors useful for the practice of the instant methods, see, Dubensky et al., *J. Virol.* (1996) 70:508-519; and International Publication Nos. WO 95/07995 and WO 96/17072; as well as, Dubensky, Jr., T.W., et al., U.S. Patent No. 5,843,723,

issued December 1, 1998, and Dubensky, Jr., T.W., U.S. Patent No. 5,789,245, issued August 4, 1998.

A vaccinia based infection/transfection system can be conveniently used to provide for inducible, transient expression of the coding sequences of interest (for example, a synthetic Gag/HCV-core expression cassette) in a host cell. In this system, cells are first infected in vitro with a vaccinia virus recombinant that encodes the bacteriophage T7 RNA polymerase. This polymerase displays exquisite specificity in that it only transcribes templates bearing T7 promoters. Following infection, cells are transfected with the polynucleotide of interest, driven by a T7 promoter. The polymerase expressed in the cytoplasm from the vaccinia virus recombinant transcribes the transfected DNA into RNA which is then translated into protein by the host translational machinery. The method provides for high level, transient, cytoplasmic production of large quantities of RNA and its translation products. See, e.g., Elroy-Stein and Moss, *Proc. Natl. Acad. Sci. USA* (1990) 87:6743-6747; Fuerst et al., *Proc. Natl. Acad. Sci. USA* (1986) 83:8122-8126.

As an alternative approach to infection with vaccinia or avipox virus recombinants, or to the delivery of genes using other viral vectors, an amplification system can be used that will lead to high level expression following introduction into host cells. Specifically, a T7 RNA polymerase promoter preceding the coding region for T7 RNA polymerase can be engineered. Translation of RNA derived from this template will generate T7 RNA polymerase which in turn will transcribe more template. Concomitantly, there will be a cDNA whose expression is under the control of the T7 promoter. Thus, some of the T7 RNA polymerase generated from

translation of the amplification template RNA will lead to transcription of the desired gene. Because some T7 RNA polymerase is required to initiate the amplification, T7 RNA polymerase can be introduced into cells along with the template(s) to prime the transcription reaction. The polymerase can be introduced as a protein or on a plasmid encoding the RNA polymerase. For a further discussion of T7 systems and their use for transforming cells, see, e.g., International Publication No. WO 94/26911; Studier and Moffatt, *J. Mol. Biol.* (1986) 189:113-130; Deng and Wolff, *Gene* (1994) 143:245-249; Gao et al., *Biochem. Biophys. Res. Commun.* (1994) 200:1201-1206; Gao and Huang, *Nuc. Acids Res.* (1993) 21:2867-2872; Chen et al., *Nuc. Acids Res.* (1994) 22:2114-2120; and U.S. Patent No. 5,135,855.

The synthetic expression cassette of interest can also be delivered without a viral vector. For example, the synthetic expression cassette can be packaged as DNA or RNA in liposomes prior to delivery to the subject or to cells derived therefrom. Lipid encapsulation is generally accomplished using liposomes which are able to stably bind or entrap and retain nucleic acid. The ratio of condensed DNA to lipid preparation can vary but will generally be around 1:1 (mg DNA:micromoles lipid), or more of lipid. For a review of the use of liposomes as carriers for delivery of nucleic acids, see, Hug and Sleight, *Biochim. Biophys. Acta.* (1991) 1097:1-17; Straubinger et al., in *Methods of Enzymology* (1983), Vol. 101, pp. 512-527.

Liposomal preparations for use in the present invention include cationic (positively charged), anionic (negatively charged) and neutral preparations, with cationic liposomes particularly preferred. Cationic liposomes have been shown to mediate intracellular

delivery of plasmid DNA (Felgner et al., *Proc. Natl. Acad. Sci. USA* (1987) 84:7413-7416); mRNA (Malone et al., *Proc. Natl. Acad. Sci. USA* (1989) 86:6077-6081); and purified transcription factors (Debs et al., *J. Biol. Chem.* (1990) 265:10189-10192), in functional form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleoyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, NY. (See, also, Felgner et al., *Proc. Natl. Acad. Sci. USA* (1987) 84:7413-7416). Other commercially available lipids include (DDAB/DOPE) and DOTAP/DOPE (Boehringer). Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, e.g., Szoka et al., *Proc. Natl. Acad. Sci. USA* (1978) 75:4194-4198; PCT Publication No. WO 90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes.

Similarly, anionic and neutral liposomes are readily available, such as, from Avanti Polar Lipids (Birmingham, AL), or can be easily prepared using readily available materials. Such materials include phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

The liposomes can comprise multilammellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs). The various liposome-nucleic acid complexes are prepared using methods known in the art. See, e.g., Straubinger et al., in METHODS OF

IMMUNOLOGY (1983), Vol. 101, pp. 512-527; Szoka et al.,
Proc. Natl. Acad. Sci. USA (1978) 75:4194-4198;
Papahadjopoulos et al., *Biochim. Biophys. Acta* (1975)
394:483; Wilson et al., *Cell* (1979) 17:77); Deamer and
5 Bangham, *Biochim. Biophys. Acta* (1976) 443:629; Ostro et
al., *Biochem. Biophys. Res. Commun.* (1977) 76:836; Fraley
et al., *Proc. Natl. Acad. Sci. USA* (1979) 76:3348); Enoch
and Strittmatter, *Proc. Natl. Acad. Sci. USA* (1979)
76:145); Fraley et al., *J. Biol. Chem.* (1980) 255:10431;
10 Szoka and Papahadjopoulos, *Proc. Natl. Acad. Sci. USA*
(1978) 75:145; and Schaefer-Ridder et al., *Science* (1982)
215:166.

The DNA and/or protein antigen(s) can also be
delivered in cochleate lipid compositions similar to
15 those described by Papahadjopoulos et al., *Biochem.*
Biophys. Acta. (1975) 394:483-491. See, also, U.S.
Patent Nos. 4,663,161 and 4,871,488.

The synthetic expression cassette of interest (e.g.,
any of the synthetic expression cassettes described in
20 Example 1) may also be encapsulated, adsorbed to, or
associated with, particulate carriers. Such carriers
present multiple copies of a selected antigen to the
immune system and promote migration, trapping and
retention of antigens in local lymph nodes. The
25 particles can be taken up by professional antigen
presenting cells such as macrophages and dendritic cells,
and/or can enhance antigen presentation through other
mechanisms such as stimulation of cytokine release.
Examples of particulate carriers include those derived
30 from polymethyl methacrylate polymers, as well as
microparticles derived from poly(lactides) and
poly(lactide-co-glycolides), known as PLG. See, e.g.,
Jeffery et al., *Pharm. Res.* (1993) 10:362-368; McGee JP,

et al., *J Microencapsul.* 14(2):197-210, 1997; O'Hagan DT, et al., *Vaccine* 11(2):149-54, 1993.

Furthermore, other particulate systems and polymers can be used for the *in vivo* or *ex vivo* delivery of the gene of interest. For example, polymers such as polylysine, polyarginine, polyornithine, spermine, spermidine, as well as conjugates of these molecules, are useful for transferring a nucleic acid of interest. Similarly, DEAE dextran-mediated transfection, calcium phosphate precipitation or precipitation using other insoluble inorganic salts, such as strontium phosphate, aluminum silicates including bentonite and kaolin, chromic oxide, magnesium silicate, talc, and the like, will find use with the present methods. See, e.g., Felgner, P.L., *Advanced Drug Delivery Reviews* (1990) 5:163-187, for a review of delivery systems useful for gene transfer. Peptoids (Zuckerman, R.N., et al., U.S. Patent No. 5,831,005, issued November 3, 1998) may also be used for delivery of a construct of the present invention.

Additionally, biolistic delivery systems employing particulate carriers such as gold and tungsten, are especially useful for delivering synthetic expression cassettes of the present invention. The particles are coated with the synthetic expression cassette(s) to be delivered and accelerated to high velocity, generally under a reduced atmosphere, using a gun powder discharge from a "gene gun." For a description of such techniques, and apparatuses useful therefore, see, e.g., U.S. Patent Nos. 4,945,050; 5,036,006; 5,100,792; 5,179,022; 5,371,015; and 5,478,744. Also, needle-less injection systems can be used (Davis, H.L., et al, *Vaccine* 12:1503-1509, 1994; Bioject, Inc., Portland, OR).

Recombinant vectors carrying a synthetic expression cassette of the present invention are formulated into compositions for delivery to the vertebrate subject. These compositions may either be prophylactic (to prevent
5 infection) or therapeutic (to treat disease after infection). The compositions will comprise a "therapeutically effective amount" of the gene of interest such that an amount of the antigen can be produced in vivo so that an immune response is generated
10 in the individual to which it is administered. The exact amount necessary will vary depending on the subject being treated; the age and general condition of the subject to be treated; the capacity of the subject's immune system to synthesize antibodies; the degree of protection
15 desired; the severity of the condition being treated; the particular antigen selected and its mode of administration, among other factors. An appropriate effective amount can be readily determined by one of skill in the art. Thus, a "therapeutically effective
20 amount" will fall in a relatively broad range that can be determined through routine trials.

The compositions will generally include one or more "pharmaceutically acceptable excipients or vehicles" such as water, saline, glycerol, polyethyleneglycol,
25 hyaluronic acid, ethanol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, surfactants and the like, may be present in such vehicles. Certain facilitators of immunogenicity or of nucleic acid uptake and/or
30 expression can also be included in the compositions or coadministered, such as, but not limited to, bupivacaine, cardiotoxin and sucrose.

Once formulated, the compositions of the invention can be administered directly to the subject (e.g., as

described above) or, alternatively, delivered ex vivo, to cells derived from the subject, using methods such as those described above. For example, methods for the ex vivo delivery and reimplantation of transformed cells
5 into a subject are known in the art and can include, e.g., dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, lipofectamine and LT-1 mediated transfection, protoplast fusion, electroporation, encapsulation of the
10 polynucleotide(s) (with or without the corresponding antigen) in liposomes, and direct microinjection of the DNA into nuclei.

Direct delivery of synthetic expression cassette compositions in vivo will generally be accomplished with
15 or without viral vectors, as described above, by injection using either a conventional syringe, needless devices such as Bioject® or a gene gun, such as the Accell® gene delivery system (PowderJect Technologies, Inc., Oxford, England). The constructs can be delivered
20 (e.g., injected) either subcutaneously, epidermally, intradermally, intramuscularly, intravenous, intramucosally (such as nasally, rectally and vaginally), intraperitoneally or orally. Delivery of DNA into cells of the epidermis is particularly preferred as this mode
25 of administration provides access to skin-associated lymphoid cells and provides for a transient presence of DNA in the recipient. Other modes of administration include oral ingestion and pulmonary administration, suppositories, needle-less injection, transcutaneous and
30 transdermal applications. Dosage treatment may be a single dose schedule or a multiple dose schedule.

2.3.2 EX VIVO DELIVERY OF THE SYNTHETIC EXPRESSION
CASSETTES OF THE PRESENT INVENTION

In one embodiment, T cells, and related cell types (including but not limited to antigen presenting cells, such as, macrophage, monocytes, lymphoid cells, dendritic cells, B-cells, T-cells, stem cells, and progenitor cells thereof), can be used for ex vivo delivery of the synthetic expression cassettes of the present invention. T cells can be isolated from peripheral blood lymphocytes (PBLs) by a variety of procedures known to those skilled in the art. For example, T cell populations can be "enriched" from a population of PBLs through the removal of accessory and B cells. In particular, T cell enrichment can be accomplished by the elimination of non-T cells using anti-MHC class II monoclonal antibodies. Similarly, other antibodies can be used to deplete specific populations of non-T cells. For example, anti-Ig antibody molecules can be used to deplete B cells and anti-MacI antibody molecules can be used to deplete macrophages.

T cells can be further fractionated into a number of different subpopulations by techniques known to those skilled in the art. Two major subpopulations can be isolated based on their differential expression of the cell surface markers CD4 and CD8. For example, following the enrichment of T cells as described above, CD4⁺ cells can be enriched using antibodies specific for CD4 (see Coligan et al., *supra*). The antibodies may be coupled to a solid support such as magnetic beads. Conversely, CD8⁺ cells can be enriched through the use of antibodies specific for CD4 (to remove CD4⁺ cells), or can be isolated by the use of CD8 antibodies coupled to a solid support. CD4

lymphocytes from HIV-1 infected patients can be expanded *ex vivo*, before or after transduction as described by Wilson et. al. (1995) *J. Infect. Dis.* 172:88.

5 Following purification of T cells, a variety of methods of genetic modification known to those skilled in the art can be performed using non-viral or viral-based gene transfer vectors constructed as described herein. For example, one such approach involves transduction of
10 the purified T cell population with vector-containing supernatant of cultures derived from vector producing cells. A second approach involves co-cultivation of an irradiated monolayer of vector-producing cells with the purified T cells. A third approach involves a similar
15 co-cultivation approach; however, the purified T cells are pre-stimulated with various cytokines and cultured 48 hours prior to the co-cultivation with the irradiated vector producing cells. Pre-stimulation prior to such transduction increases effective gene transfer (Nolta et
20 al. (1992) *Exp. Hematol.* 20:1065). Stimulation of these cultures to proliferate also provides increased cell populations for re-infusion into the patient. Subsequent to co-cultivation, T cells are collected from the vector producing cell monolayer, expanded, and frozen in liquid
25 nitrogen.

 Gene transfer vectors, containing one or more synthetic expression cassette of the present invention (associated with appropriate control elements for delivery to the isolated T cells) can be assembled using
30 known methods.

 Selectable markers can also be used in the construction of gene transfer vectors. For example, a marker can be used which imparts to a mammalian cell transduced with the gene transfer vector resistance to a

cytotoxic agent. The cytotoxic agent can be, but is not limited to, neomycin, aminoglycoside, tetracycline, chloramphenicol, sulfonamide, actinomycin, netropsin, distamycin A, anthracycline, or pyrazinamide. For
5 example, neomycin phosphotransferase II imparts resistance to the neomycin analogue geneticin (G418).

The T cells can also be maintained in a medium containing at least one type of growth factor prior to being selected. A variety of growth factors are known in
10 the art which sustain the growth of a particular cell type. Examples of such growth factors are cytokine mitogens such as rIL-2, IL-10, IL-12, and IL-15, which promote growth and activation of lymphocytes. Certain types of cells are stimulated by other growth factors
15 such as hormones, including human chorionic gonadotropin (hCG) and human growth hormone. The selection of an appropriate growth factor for a particular cell population is readily accomplished by one of skill in the art.

20 For example, white blood cells such as differentiated progenitor and stem cells are stimulated by a variety of growth factors. More particularly, IL-3, IL-4, IL-5, IL-6, IL-9, GM-CSF, M-CSF, and G-CSF, produced by activated T_H and activated macrophages,
25 stimulate myeloid stem cells, which then differentiate into pluripotent stem cells, granulocyte-monocyte progenitors, eosinophil progenitors, basophil progenitors, megakaryocytes, and erythroid progenitors. Differentiation is modulated by growth factors such as
30 GM-CSF, IL-3, IL-6, IL-11, and EPO.

Pluripotent stem cells then differentiate into lymphoid stem cells, bone marrow stromal cells, T cell progenitors, B cell progenitors, thymocytes, T_H Cells, T_c cells, and B cells. This differentiation is modulated by

growth factors such as IL-3, IL-4, IL-6, IL-7, GM-CSF, M-CSF, G-CSF, IL-2, and IL-5.

Granulocyte-monocyte progenitors differentiate to monocytes, macrophages, and neutrophils. Such
5 differentiation is modulated by the growth factors GM-CSF, M-CSF, and IL-8. Eosinophil progenitors differentiate into eosinophils. This process is modulated by GM-CSF and IL-5.

The differentiation of basophil progenitors into
10 mast cells and basophils is modulated by GM-CSF, IL-4, and IL-9. Megakaryocytes produce platelets in response to GM-CSF, EPO, and IL-6. Erythroid progenitor cells differentiate into red blood cells in response to EPO.

Thus, during activation by the CD3-binding agent, T
15 cells can also be contacted with a mitogen, for example a cytokine such as IL-2. In particularly preferred embodiments, the IL-2 is added to the population of T cells at a concentration of about 50 to 100 $\mu\text{g/ml}$. Activation with the CD3-binding agent can be carried out
20 for 2 to 4 days.

Once suitably activated, the T cells are genetically modified by contacting the same with a suitable gene transfer vector under conditions that allow for transfection of the vectors into the T cells. Genetic
25 modification is carried out when the cell density of the T cell population is between about 0.1×10^6 and 5×10^6 , preferably between about 0.5×10^6 and 2×10^6 . A number of suitable viral and nonviral-based gene transfer vectors have been described for use herein.

30 After transduction, transduced cells are selected away from non-transduced cells using known techniques. For example, if the gene transfer vector used in the transduction includes a selectable marker which confers resistance to a cytotoxic agent, the cells can be

contacted with the appropriate cytotoxic agent, whereby non-transduced cells can be negatively selected away from the transduced cells. If the selectable marker is a cell surface marker, the cells can be contacted with a binding agent specific for the particular cell surface marker, whereby the transduced cells can be positively selected away from the population. The selection step can also entail fluorescence-activated cell sorting (FACS) techniques, such as where FACS is used to select cells from the population containing a particular surface marker, or the selection step can entail the use of magnetically responsive particles as retrievable supports for target cell capture and/or background removal.

More particularly, positive selection of the transduced cells can be performed using a FACS cell sorter (e.g. a FACSVantage™ Cell Sorter, Becton Dickinson Immunocytometry Systems, San Jose, CA) to sort and collect transduced cells expressing a selectable cell surface marker. Following transduction, the cells are stained with fluorescent-labeled antibody molecules directed against the particular cell surface marker. The amount of bound antibody on each cell can be measured by passing droplets containing the cells through the cell sorter. By imparting an electromagnetic charge to droplets containing the stained cells, the transduced cells can be separated from other cells. The positively selected cells are then harvested in sterile collection vessels. These cell sorting procedures are described in detail, for example, in the FACSVantage™ Training Manual, with particular reference to sections 3-11 to 3-28 and 10-1 to 10-17.

Positive selection of the transduced cells can also be performed using magnetic separation of cells based on expression of a particular cell surface marker. In such

separation techniques, cells to be positively selected are first contacted with specific binding agent (e.g., an antibody or reagent that interacts specifically with the cell surface marker). The cells are then contacted with
5 retrievable particles (e.g., magnetically responsive particles) which are coupled with a reagent that binds the specific binding agent (that has bound to the positive cells). The cell-binding agent-particle complex can then be physically separated from non-labeled cells,
10 for example using a magnetic field. When using magnetically responsive particles, the labeled cells can be retained in a container using a magnetic field while the negative cells are removed. These and similar separation procedures are known to those of ordinary
15 skill in the art.

Expression of the vector in the selected transduced cells can be assessed by a number of assays known to those skilled in the art. For example, Western blot or Northern analysis can be employed depending on the nature
20 of the inserted nucleotide sequence of interest. Once expression has been established and the transformed T cells have been tested for the presence of the selected synthetic expression cassette, they are ready for infusion into a patient via the peripheral blood stream.

25 The invention includes a kit for genetic modification of an *ex vivo* population of primary mammalian cells. The kit typically contains a gene transfer vector coding for at least one selectable marker and at least one synthetic expression cassette contained
30 in one or more containers, ancillary reagents or hardware, and instructions for use of the kit.

EXPERIMENTAL

Below are examples of specific embodiments for carrying out the present invention. The examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

Efforts have been made to ensure accuracy with respect to numbers used (e.g., amounts, temperatures, etc.), but some experimental error and deviation should, of course, be allowed for.

Example 1Generation of Synthetic Gag and Env Expression Cassettes

A. Modification of HIV-1 Gag, Gag-protease, Gag-reverse transcriptase and Gag-polymerase Nucleic Acid Coding Sequences

The Gag (SEQ ID NO:1), Gag-protease (SEQ ID NO:2), Gag-polymerase (SEQ ID NO:3), and Gag-reverse transcriptase (SEQ ID NO:77) coding sequences were selected from the HIV-1SF2 strain (Sanchez-Pescador, R., et al., *Science* 227(4686): 484-492, 1985; Luciw, P.A., et al. U.S. Patent No. 5,156,949, issued October 20, 1992; Luciw, P.A., et al., U.S. Patent No. 5,688,688, November 18, 1997). These sequences were manipulated to maximize expression of their gene products.

First, the HIV-1 codon usage pattern was modified so that the resulting nucleic acid coding sequence was comparable to codon usage found in highly expressed human genes. The HIV codon usage reflects a high content of the nucleotides A or T of the codon-triplet. The effect of the HIV-1 codon usage is a high AT content in the DNA sequence that results in a high AU content in the RNA and in a decreased translation ability and instability of the

mRNA. In comparison, highly expressed human codons prefer the nucleotides G or C. The Gag-encoding sequences were modified to be comparable to codon usage found in highly expressed human genes.

5 Figure 11 presents a comparison of the percent A-T content for the cDNAs of stable versus unstable RNAs (comparison window size = 50). Human IFN γ mRNA is known to (i) be unstable, (ii) have a short half-life, and (iii) have a high A-U content. Human GAPDH
10 (glyceraldehyde-3-phosphate dehydrogenase) mRNA is known to (i) be a stable RNA, and (i) have a low A-U content. In Figure 11, the percent A-T content of these two sequences are compared to the percent A-T content of native HIV-1SF2 Gag cDNA and to the synthetic Gag cDNA
15 sequence of the present invention. The top two panels of the figure show the percent A-T content over the length of the sequences for IFN γ and native Gag. The bottom two panels of the figure show the percent A-T content over the length of the sequences for GAPDH and the synthetic
20 Gag. Experiments performed in support of the present invention showed that the synthetic Gag sequences were capable of higher level of protein production (see the Examples) than the native Gag sequences. The data in Figure 11 suggest that one reason for this increased
25 production may be increased stability of the mRNA corresponding to the synthetic Gag coding sequences versus the mRNA corresponding to the native Gag coding sequences.

 Second, there are inhibitory (or instability)
30 elements (INS) located within the coding sequences of the Gag and Gag-protease coding sequences (Schneider R, et al., *J Virol.* 71(7):4892-4903, 1997). RRE is a secondary RNA structure that interacts with the HIV encoded Rev-protein to overcome the expression down-regulating

effects of the INS. To overcome the requirement for post-transcriptional activating mechanisms of RRE and Rev, and to enhance independent expression of the Gag polypeptide, the INS were inactivated by introducing multiple point mutations that did not alter the reading frame of the encoded proteins. Figure 1 shows the original SF2 Gag sequence, the location of the INS sequences, and the modifications made to the INS sequences to reduce their effects.

For the Gag-protease sequence (wild type, SEQ ID NO:2; synthetic, SEQ ID NOs:5, 78 and 79), the changes in codon usage were restricted to the regions up to the -1 frameshift and starting again at the end of the Gag reading frame (Figure 2; the region indicated in lower case letters in Figure 2 is the unmodified region). Further, inhibitory (or instability) elements (INS) located within the coding sequences of the Gag-protease polypeptide coding sequence were altered as well (indicated in Figure 2). The synthetic coding sequences were assembled by the Midland Certified Reagent Company (Midland, Texas).

Modification of the Gag-polymerase sequences (wild type, SEQ ID NO:3; synthetic, SEQ ID NO:6) and Gag-reverse transcriptase sequences (SEQ ID NOs:80 through 84) include similar modifications as described for Gag-protease in order to preserve the frameshift region. Locations of the inactivation sites and changes to the sequence to alter the inactivation sites are presented in Figure 12 for the native HIV-1_{SF2} Gag-polymerase sequence.

In one embodiment of the invention, the full length polymerase coding region of the Gag-polymerase sequence is included with the synthetic Gag sequences in order to increase the number of epitopes for virus-like particles expressed by the synthetic, optimized Gag expression

cassette. Because synthetic HIV-1 Gag-polymerase expresses the potentially deleterious functional enzymes reverse transcriptase (RT) and integrase (INT) (in addition to the structural proteins and protease), it is important to inactivate RT and INT functions. Several in-frame deletions in the RT and INT reading frame can be made to achieve catalytic nonfunctional enzymes with respect to their RT and INT activity. {Jay. A. Levy (Editor) (1995) *The Retroviridae*, Plenum Press, New York. ISBN 0-306-45033X. Pages 215-20; Grimison, B. and Laurence, J. (1995), *Journal Of Acquired Immune Deficiency Syndromes and Human Retrovirology* 9(1):58-68; Wakefield, J. K., et al., (1992) *Journal Of Virology* 66(11):6806-6812; Esnouf, R., et al., (1995) *Nature Structural Biology* 2(4):303-308; Maignan, S., et al., (1998) *Journal Of Molecular Biology* 282(2):359-368; Katz, R. A. and Skalka, A. M. (1994) *Annual Review Of Biochemistry* 73 (1994); Jacobo-Molina, A., et al., (1993) *Proceedings Of the National Academy Of Sciences Of the United States Of America* 90(13):6320-6324; Hickman, A. B., et al., (1994) *Journal Of Biological Chemistry* 269(46):29279-29287; Goldgur, Y., et al., (1998) *Proceedings Of the National Academy Of Sciences Of the United States Of America* 95(16):9150-9154; Goette, M., et al., (1998) *Journal Of Biological Chemistry* 273(17):10139-10146; Gorton, J. L., et al., (1998) *Journal of Virology* 72(6):5046-5055; Engelman, A., et al., (1997) *Journal Of Virology* 71(5):3507-3514; Dyda, F., et al., *Science* 266(5193):1981-1986; Davies, J. F., et al., (1991) *Science* 252(5002):88-95; Bujacz, G., et al., (1996) *Febs Letters* 398(2-3):175-178; Beard, W. A., et al., (1996) *Journal Of Biological Chemistry* 271(21):12213-12220; Kohlstaedt, L. A., et al., (1992)

Science 256(5065):1783-1790; Krug, M. S. and Berger, S. L. (1991) *Biochemistry* 30(44):10614-10623; Mazumder, A., et al., (1996) *Molecular Pharmacology* 49(4):621-628; Palaniappan, C., et al., (1997) *Journal Of Biological Chemistry* 272(17):11157-11164; Rodgers, D. W., et al., (1995) *Proceedings Of the National Academy Of Sciences Of the United States Of America* 92(4):1222-1226; Sheng, N. and Dennis, D. (1993) *Biochemistry* 32(18):4938-4942; Spence, R. A., et al., (1995) *Science* 267(5200):988-993.

Furthermore selected B- and/or T-cell epitopes can be added to the Gag-polymerase constructs within the deletions of the RT- and INT-coding sequence to replace and augment any epitopes deleted by the functional modifications of RT and INT. Alternately, selected B- and T-cell epitopes (including CTL epitopes) from RT and INT can be included in a minimal VLP formed by expression of the synthetic Gag or synthetic GagProt cassette, described above. (For descriptions of known HIV B- and T-cell epitopes see, HIV Molecular Immunology Database CTL Search Interface; Los Alamos Sequence Compendia, 1987-1997; Internet address: <http://hiv-web.lanl.gov/immunology/index.html>.)

The resulting modified coding sequences are presented as a synthetic Gag expression cassette (SEQ ID NO:4), a synthetic Gag-protease expression cassette (SEQ ID NOs:5, 78 and 79), and a synthetic Gag-polymerase expression cassette (SEQ ID NO:6). Synthetic expression cassettes containing codon modifications in the reverse transcriptase region are shown in SEQ ID NOs:80 through 84. An alignment of selected sequences is presented in Figure 7. A common region (Gag-common; SEQ ID NO:9) extends from position 1 to position 1262.

The synthetic DNA fragments for Gag and Gag-protease were cloned into the following expression vectors:

pCMVKm2, for transient expression assays and DNA immunization studies, the pCMVKm2 vector was derived from pCMV6a (Chapman et al., *Nuc. Acids Res.* (1991) 19:3979-3986) and comprises a kanamycin selectable marker, a
5 ColE1 origin of replication, a CMV promoter enhancer and Intron A, followed by an insertion site for the synthetic sequences described below followed by a polyadenylation signal derived from bovine growth hormone -- the pCMVKm2 vector differs from the pCMV-link vector only in that a
10 polylinker site was inserted into pCMVKm2 to generate pCMV-link (Figure 14, polylinker at positions 1646 to 1697); pESN2dhfr (Figure 13A) and pCMVPLEdhfr (also known as pCMVIII as shown in Figure 13B), for expression in Chinese Hamster Ovary (CHO) cells; and, pAcC13, a shuttle
15 vector for use in the Baculovirus expression system (pAcC13, was derived from pAcC12 which was described by Munemitsu S., et al., *Mol Cell Biol.* 10(11):5977-5982, 1990).

A restriction map for vector pCMV-link is presented
20 in Figure 14. In the figure, the CMV promoter (CMV IE ENH/PRO), bovine growth hormone terminator (BGH pA), kanamycin selectable marker (kan), and a ColE1 origin of replication (ColE1 ori) are indicated. A polycloning site is also indicated in the figure following the CMV
25 promoter sequences.

A restriction map for vector pESN2dhfr is presented in Figure 13A. In the figure, the CMV promoter (pCMV, hCMVIE), bovine growth hormone terminator (BGHpA), SV40 origin of replication (SV40ori), neomycin selectable
30 marker (Neo), SV40 polyA (SV40pA), Adenovirus 2 late promoter (Ad2VLP), and the murine dhfr gene (mu dhfr) are indicated. A polycloning site is also indicated in the figure following the CMV promoter sequences.

Briefly, construction of pCMVPLEdhfr (pCMVIII) was as follows. To construct a DHFR cassette, the EMCV IRES (internal ribosome entry site) leader was PCR-amplified from pCite-4a+ (Novagen, Inc., Milwaukee, WI) and
5 inserted into pET-23d (Novagen, Inc., Milwaukee, WI) as an *Xba*-*Nco* fragment to give pET-EMCV. The *dhfr* gene was PCR-amplified from pESN2dhfr to give a product with a Gly-Gly-Gly-Ser spacer in place of the translation stop codon and inserted as an *Nco*-*Bam*H1 fragment to give pET-
10 E-DHFR. Next, the attenuated *neo* gene was PCR amplified from a pSV2Neo (Clontech, Palo Alto, CA) derivative and inserted into the unique *Bam*H1 site of pET-E-DHFR to give pET-E-DHFR/*Neo*_(m2). Then, the bovine growth hormone terminator from pCDNA3 (Invitrogen, Inc., Carlsbad, CA)
15 was inserted downstream of the *neo* gene to give pET-E-DHFR/*Neo*_(m2)BGHT. The EMCV-*dhfr/neo* selectable marker cassette fragment was prepared by cleavage of pET-E-DHFR/*Neo*_(m2)BGHT. The CMV enhancer/promoter plus Intron A was transferred from pCMV6a (Chapman et al., *Nuc. Acids*
20 *Res.* (1991) 19:3979-3986) as a *Hind*III-*Sal*I fragment into pUC19 (New England Biolabs, Inc., Beverly, MA). The vector backbone of pUC19 was deleted from the *Nde*I to the *Sap*I sites. The above described DHFR cassette was added to the construct such that the EMCV IRES followed the CMV
25 promoter to produce the final construct. The vector also contained an *amp*^r gene and an SV40 origin of replication.

Selected pCMVKm2 vectors containing the synthetic expression cassettes have been designated as follows: pCMVKm2.GagMod.SF2, pCMVKm2.GagprotMod.SF2, and
30 pCMVKm2.GagpolMod.SF2, pCMVKm2.GagprotMod.SF2.GP1 (SEQ ID NO:78) and pCMVKm2.GagprotMod.SF2.GP2 (SEQ ID NO:79). Other exemplary Gag-encoding expressing cassettes are shown in the Figures and as Sequence Listings.

B. Modification of HIV-1 Gag/Hepatitis C Core Chimeric Protein Nucleic Acid Coding Sequences Generation of Synthetic Expression Cassettes

To facilitate the ligation of the Gag and HCV core coding sequences, PCR amplification was employed. The synthetic p55Gag expression cassette was used as a PCR template with the following primers: GAG5 (SEQ ID NO:11) and P55-SAL3 (SEQ ID NO:12). The PCR amplification was conducted at 55°C for 25 cycles using Stratagene's Pfu polymerase. The resulting PCR product was rendered free of nucleotides and primers using the Promega PCR clean-up kit and then subjected to EcoRI and SalI digestions. For HCV core coding sequences, the following primers were used with an HCV template (Houghton, M., et al., U.S. Patent No. 5,714,596, issued February 3, 1998; Houghton, M., et al., U.S. Patent No. 5,712,088, issued January 27, 1998; Houghton, M., et al., U.S. Patent No. 5,683,864, issued November 4, 1997; Weiner, A.J., et al., U.S. Patent No. 5,728,520, issued March 17, 1998; Weiner, A.J., et al., U.S. Patent No. 5,766,845, issued June 16, 1998; Weiner, A.J., et al., U.S. Patent No. 5,670,152, issued September 23, 1997): CORESAL 5 (SEQ ID NO:13) and 173CORE (SEQ ID NO:14) using the conditions outlined above. The purified product was digested with SalI and BamHI restriction enzymes. The digested Gag and HCV core PCR products were ligated into the pCMVKm2 vector digested with EcoRI and BamHI. Ligation of the PCR products at the SalI site resulted in a direct fusion of the final amino acid of p55Gag to the second amino acid of HCV core, serine. Amino acid 173 of core is a serine and is followed immediately by a TAG termination codon. The sequence of the fusion clone was confirmed. The pCMVKm2 vector containing the synthetic expression

cassette was designated as pCMVKm2.GagModHCVcore.

The EcoRI-BamHI fragment of p55Gag-core 173 was also cloned into EcoRI-BamHI-digested pAcC13 for baculovirus expression. Western blots confirmed expression and sucrose gradient sedimentation along with electron microscopy confirmed particle formation. To generate the above clone but containing the synthetic Gag sequences (instead of wild-type), the following steps were performed: pCMVKm2-modified p55Gag was used as template for PCR amplification with MS65 (SEQ ID NO:15) and MS66 (SEQ ID NO:16) primers. The region amplified corresponds to the BspHI and SalI sites at the C-terminus of synthetic Gag sequence. The amplification product was digested with BspHI and SalI and ligated to SalI/BamHI digested pCMV-link along with the Sal/BspHI fragment from pCMV-Km-p55modGag, representing the amino terminal end of modified Gag, and the SalI/BamHI fragment from pCMV-p55Gag-core173. Thereafter, a T4-blunted-SalI partial/BamHI fragment was ligated into pAcC4-SmaI/BamHI to generate pAcC4-p55GagMod-core173 (containing the synthetic sequence presented as SEQ ID NO:7).

C. Defining of the Major Homology Region (MHR) of HIV-1 p55Gag

The Major Homology Region (MHR) of HIV-1 p55 (Gag) is located in the p24-CA sequence of Gag. It is a conserved stretch of 20 amino acids (SEQ ID NO:19). The position in the wild type HIV-1_{SF2} Gag protein is from aa 286-305 and spans a region from nucleotides 856-915 in the native HIV-1_{SF2} Gag DNA-sequence. The position in the synthetic Gag protein is from aa 288-307 and spans a region from nucleotides 862-921 for the synthetic Gag DNA-sequence. The nucleotide sequence for the MHR in the synthetic

GagMod.SF2 is presented as SEQ ID NO:20. Mutations or deletions in the amino acid sequence of the MHR can severely impair particle production (Borsetti, A., et al., *J. Virol.* 72(11):9313-9317, 1998; Mammano, F., et al., *J Virol* 68(8):4927-4936, 1994).

Percent identity to the MHR nucleotide sequence can be determined, for example, using the MacDNAsis program (Hitachi Software Engineering America Limited, South San Francisco, CA), Higgins algorithm, with the following exemplary parameters: gap penalty = 5, no. of top diagonals = 5, fixed gap penalty = 5, K-tuple = 2, window size = 5, and floating gap penalty = 10.

D. Generation of Synthetic Env Expression Cassettes

Env coding sequences of the present invention include, but are not limited to, polynucleotide sequences encoding the following HIV-encoded polypeptides: gp160, gp140, and gp120 (see, e.g., U.S. Patent No. 5,792,459 for a description of the HIV-1_{SF2} ("SF2") Env polypeptide). The relationships between these polypeptides is shown schematically in Figure 15 (in the figure: the polypeptides are indicated as lines, the amino and carboxy termini are indicated on the gp160 line; the open circle represents the oligomerization domain; the open square represents a transmembrane spanning domain (TM); and "c" represents the location of a cleavage site, in gp140.mut the "X" indicates that the cleavage site has been mutated such that it no longer functions as a cleavage site). The polypeptide gp160 includes the coding sequences for gp120 and gp41. The polypeptide gp41 is comprised of several domains including an oligomerization domain (OD) and a transmembrane spanning domain (TM). In the native envelope, the oligomerization domain is required for the

non-covalent association of three gp41 polypeptides to form a trimeric structure: through non-covalent interactions with the gp41 trimer (and itself), the gp120 polypeptides are also organized in a trimeric structure.

5 A cleavage site (or cleavage sites) exists approximately between the polypeptide sequences for gp120 and the polypeptide sequences corresponding to gp41. This cleavage site(s) can be mutated to prevent cleavage at the site. The resulting gp140 polypeptide corresponds to

10 a truncated form of gp160 where the transmembrane spanning domain of gp41 has been deleted. This gp140 polypeptide can exist in both monomeric and oligomeric (i.e. trimeric) forms by virtue of the presence of the oligomerization domain in the gp41 moiety. In the

15 situation where the cleavage site has been mutated to prevent cleavage and the transmembrane portion of gp41 has been deleted the resulting polypeptide product is designated "mutated" gp140 (e.g., gp140.mut). As will be apparent to those in the field, the cleavage site can be

20 mutated in a variety of ways. The native amino acid sequence in the SF162 cleavage sites is: APTKAKRRVVQREKR (SEQ ID NO:21), where KAKRR (SEQ ID NO:22) is termed the "second" site and REKR (SEQ ID NO:23) is the "first site". Exemplary mutations include the following

25 constructs: gp140.mut7.modSF162 which encodes the amino acid sequence APTKAISSVVQSEKS (SEQ ID NO:24) in the cleavage site region; gp140.mut8.modSF162 which encodes the amino acid sequence APTIAISSVVQSEKS (SEQ ID NO:25) in the cleavage site region and gp140mut.modSF162 which

30 encodes the amino acid sequence APTKAKRRVVQREKS (SEQ ID NO:26). Mutations are denoted in bold. The native amino acid sequence in the US4 cleavage sites is: APTQAKRRVVQREKR (SEQ ID NO:27), where QAKRR (SEQ ID NO:28) is termed the "second" site and REKR (SEQ ID

NO:23) is the "first site". Exemplary mutations include the following construct: gp140.mut.modUS4 which encodes the amino acid sequence APTQAKRRVVQREKS (SEQ ID NO:29) in the cleavage site region. Mutations are denoted in bold.

5

E. Modification of HIV-1 Env (Envelope) Nucleic Acid Coding Sequences

In one embodiment of the present invention, wild-type Env coding sequences were selected from the HIV-1^{SF162} ("SF162") strain (Cheng-Mayer (1989) *PNAS USA* 86:8575-8579). These SF162 sequences were as follows: gp120, SEQ ID NO:30 (Fig. 16); gp140, SEQ ID NO:31 (Fig. 17); and gp160, SEQ ID NO:32 (Fig. 18).

In another embodiment of the present invention, wild-type Env coding sequences were selected from the HIV-US4 strain (Mascola, et al. (1994) *J. Infect. Dis.* 169:48-54). These US4 sequences were as follows: gp120, SEQ ID NO:51 (Fig. 38); gp140, SEQ ID NO:52 (Fig. 39); and gp160, SEQ ID NO:53 (Fig. 40).

These Env coding sequences were manipulated to maximize expression of their gene products.

First, the wild-type coding region was modified in one or more of the following ways. In one embodiment, sequences encoding hypervariable regions of Env, particularly V1 and/or V2 were deleted. In other embodiments, mutations were introduced into sequences encoding the cleavage site in Env to abrogate the enzymatic cleavage of oligomeric gp140 into gp120 monomers. (See, e.g., Earl et al. (1990) *PNAS USA* 87:648-652; Earl et al. (1991) *J. Virol.* 65:31-41). In yet other embodiments, hypervariable region(s) were deleted, N-glycosylation sites were removed and/or cleavage sites mutated.

Second, the HIV-1 codon usage pattern was modified

so that the resulting nucleic acid coding sequence was comparable to codon usage found in highly expressed human genes. The HIV codon usage reflects a high content of the nucleotides A or T in the codon-triplet. The effect of
5 the HIV-1 codon usage is a high AT content in the DNA sequence that results in a decreased translation ability and instability of the mRNA. In comparison, highly expressed human codons prefer the nucleotides G or C. The Env coding sequences were modified to be comparable
10 to codon usage found in highly expressed human genes.

Figures 22A-22H present comparisons of the percent A-T content for the cDNAs of stable versus unstable RNAs (comparison window size = 50). Human IFN γ mRNA is known to (i) be unstable, (ii) have a short half-life, and
15 (iii) have a high A-U content. Human GAPDH (glyceraldehyde-3-phosphate dehydrogenase) mRNA is known to (i) be a stable RNA, and (i) have a low A-U content. In Figures 22A-H, the percent A-T content of these two sequences are compared to the percent A-T content of (1)
20 native HIV-1 US4 Env gp160 cDNA, a synthetic US4 Env gp160 cDNA sequence (i.e., having modified codons) of the present invention; and (2) native HIV-1 SF162 Env gp160 cDNA, a synthetic SF162 Env gp160 cDNA sequence (i.e., having modified codons) of the present invention.
25 Figures 22A-H show the percent A-T content over the length of the sequences for IFN γ (Figures 22C and 22G); native gp160 Env US4 and SF162 (Figures 22A and 22E, respectively); GAPDH (Figures 22D and 22H); and the synthetic gp160 Env for US4 and SF162 (Figures 22B and
30 22F). Experiments performed in support of the present invention showed that the synthetic Env sequences were capable of higher level of protein production (see the Examples) than the native Env sequences. The data in Figures 22A-H suggest that one reason for this increased

production is increased stability of the mRNA corresponding to the synthetic Env coding sequences versus the mRNA corresponding to the native Env coding sequences.

5 To create the synthetic coding sequences of the present invention the gene cassettes were designed to comprise the entire coding sequence of interest. Synthetic gene cassettes were constructed by oligonucleotide synthesis and PCR amplification to
10 generate gene fragments. Primers were chosen to provide convenient restriction sites for subcloning. The resulting fragments were then ligated to create the entire desired sequence which was then cloned into an appropriate vector. The final synthetic sequences were
15 (i) screened by restriction endonuclease digestion and analysis, (ii) subjected to DNA sequencing in order to confirm that the desired sequence had been obtained and (iii) the identity and integrity of the expressed protein confirmed by SDS-PAGE and Western blotting (See,
20 Examples. The synthetic coding sequences were assembled at Chiron Corp. or by the Midland Certified Reagent Company (Midland, Texas).

 Exemplary modified coding sequences are presented as synthetic Env expression cassettes in Table 1A and 1B.
25 The following expression cassettes (i) have unique, terminal *EcoRI* and *XbaI* cloning sites; (ii) include Kozak sequences to promote optimal translation; (iii) tPA signal sequences (to direct the ENV polypeptide to the cell membrane, see, e.g., Chapman et al., *infra*); (iv)
30 open reading frames optimized for expression in mammalian cells; and (v) a translational stop signal codon.

Table 1A: Exemplary Synthetic Env Expression
Cassettes (SF162)

	Expression Cassette	Seq Id	Further Information
5	gp120 SF162	30	wild-type; Figure 16
	gp140 SF162	31	wild-type; Figure 17
	gp160 SF162	32	wild-type; Figure 18
	gp120.modSF162	33	none; Figure 19
	gp120.modSF162.delV2	34	deleted V2 loop; Figure 20
10	gp120.modSF162.delV1/V2	35	deleted V1 and V2; Figure 21
	gp140.modSF162	36	none; Figure 23
	gp140.modSF162.delV2	37	deleted V2 loop; Figure 24
	gp140.modSF162.delV1/V2	38	deleted V1 and V2; Figure 25
	gp140.mut.modSF162	39	mutated cleavage site; Fig. 26
15	gp140.mut.modSF162.delV2	40	deleted V2; mutated cleavage site; Figure 27
	gp140.mut.modSF162.delV1/V 2	41	deleted V1 & V2; mutated cleavage site; Figure 28
	gp140.mut7.modSF162	42	mutated cleavage site; Fig. 29
	gp140.mut7.modSF162.delV2	43	mutated cleavage site; deleted V2; Figure 30
20	gp140.mut7.modSF162.delV1/ V2	44	mutated cleavage site; deleted V1 and V2; Figure 31
	gp140.mut8.modSF162	45	mutated cleavage site; Fig. 32
	gp140.mut8.modSF162.delV2	46	mutated cleavage site; deleted V2; Figure 33
25	gp140.mut8.modSF162.delV1/ V2	47	mutated cleavage site; deleted V1 and V2; Figure 34
	gp160.modSF162	48	none; Figure 35
	gp160.modSF162.delV2	49	deleted V2 loop; Figure 36
	gp160.modSF162.delV1/V2	50	deleted V1 & V2; Figure 37

Table 1B:
Exemplary Synthetic Env Expression Cassettes (US4)

Expression Cassette	Seq Id	Further Information
gp120 US4	51	wild-type; Figure 38
gp140 US4	52	wild-type; Figure 39
gp160 US4	53	wild-type; Figure 40
gp120.modUS4	54	none; Figure 41
gp120.modUS4.del 128-194	55	deletion in V1 and V2 regions; Figure 42
gp140.modUS4	56	none; Figure 43
gp140.mut.modUS4	57	mutated cleavage site; Figure 44
gp140TM.modUS4	58	native transmembrane region; Figure 45
gp140.modUS4.delV1/V2	59	deleted V1 and V2; Figure 46
gp140.modUS4.delV2	60	deleted V1; Figure 47
gp140.mut.modUS4.delV1/V2	61	mutated cleavage site; deleted V1 and V2; Figure 48
gp140.modUS4.del 128-194	62	deletion in V1 and V2 regions; Figure 49
gp140.mut.modUS4.del 128-194	63	mutated cleavage site; deletion in V1 and V2 regions; Figure 50
gp160.modUS4	64	none; Figure 51
gp160.modUS4.delV1	65	deleted V1; Figure 52
gp160.modUS4.delV2	66	deleted V2; Figure 53
gp160.modUS4.delV1/V2	67	deleted V1 and V2; Figure 54
gp160.modUS4del 128-194	68	deletion in V1 and V2 regions; Figure 55

Alignments of the sequences presented in the above
tables are presented in Figures 66A and 66B.

A common region (Env-common) extends from nucleotide
position 1186 to nucleotide position 1329 (SEQ ID NO:69,

Fig. 56) relative to the wild-type US4 sequence and from nucleotide position 1117 to position 1260 (SEQ ID NO:79, Fig. 57) relative to the wild-type SF162 sequence. The synthetic sequences of the present invention

5 corresponding to these regions are presented, as SEQ ID NO:71 (Figure 58) for the synthetic Env US4 common region and as SEQ ID NO:72 (Figure 59) for the synthetic Env SF162 common region.

Percent identity to this sequence can be determined, for example, using the Smith-Waterman search algorithm (Time Logic, Incline Village, NV), with the following exemplary parameters: weight matrix = nuc4x4hb; gap opening penalty = 20, gap extension penalty = 5, reporting threshold = 1; alignment threshold = 20.

15 Various forms of the different embodiments of the present invention (e.g., constructs) may be combined.

F. Cloning Synthetic Env Expression Cassettes of the Present Invention.

20 The synthetic DNA fragments encoding the Env polypeptides were typically cloned into the eucaryotic expression vectors described above for Gag, for example, pCMVKm2/pCMVlink (Figure 4), pCMV6a, pESN2dhfr (Figure 13A), pCMVIII (Figure 13B; alternately designated as the pCMV-PL-E-dhfr/neo vector).

Exemplary designations for pCMVlink vectors containing synthetic expression cassettes of the present invention are as follows: pCMVlink.gp140.modSF162; pCMVlink.gp140.-modSF162.delV2; 30 pCMVlink.gp140.mut.modSF162; pCMVlink.gp140.mut.modSF162.delV2; pCMVKm2.gp140modUS4; pCMVKm2.gp140.modUS4.delV2; pCMVKm2.gp140.mut.modUS4; and, pCMVKm2.gp140.mut.modUS4.delV1/V2.

G. Generation of Synthetic Tat Expression Cassettes

Tat coding sequences have also been modified according to the teachings of the present specification. The wild type nucleotide sequence encoding tat from variant SF162 is presented in Figure 76 (SEQ ID NO:85). The corresponding wild-type amino acid sequence is presented in Figure 77 (SEQ ID NO:86). Figure 81 (SEQ ID NO:89) shows the nucleotide sequence encoding the amino terminal of the tat protein and the codon encoding cystein-22 is underlined. Other exemplary constructs encoding synthetic tat polypeptides are shown in Figures 78 and 79 (SEQ ID NOs:87 and 88). In one embodiment (SEQ ID NO:88), the cystein residue at position 22 is replaced by a glycine. Caputo et al. (1996) *Gene Therapy* 3:235 have shown that this mutation affects the trans activation domain of Tat.

Various forms of the different embodiments of the invention, described herein, may be combined.

H. Deposit of Vectors

Selected exemplary constructs shown below and described herein are deposited at Chiron Corporation, Emeryville, CA, 94662-8097, and were sent to the American Type Culture Collection, 10801 University Boulevard, Manassas, VA 20110-2209 on December 27, 1999.

	Plasmid Name	Chiron Deposit #	Date Sent to ATCC
	pCMVgpl60.modUS4	5094	27 Dec 99
	pCMVgpl60del1.modUS4	5095	27 Dec 99
	pCMVgpl60del2.modUS4	5096	27 Dec 99
5	pCMVgpl60del-2.modUS4	5097	27 Dec 99
	pCMVgpl60del128-194.mod.US4	5098	27 Dec 99
	pCMVgpl40mut.modUS4del128-194	5100	27 Dec 99
	pCMVgpl40.mut.mod.US	5101	27 Dec 99
	pCMVgpl60.modSF162	5125	27 Dec 99
10	pCMVgpl60.modSF162.delV2	5126	27 Dec 99
	pCMVgpl60.modSF162.delV1V2	5127	27 Dec 99
	pCMVgpl40.mut.modSF162delV2	5128	27 Dec 99
	pCMVgpl40.mut7.modSF162	5129	27 Dec 99
	pCMVgpl40.mut7.modSF162delV2	5130	27 Dec 99
15	pCMVgpl40.mut8.modSF162	5131	27 Dec 99
	pCMVgpl40.mut8.modSF162delV2	5132	27 Dec 99
	pCMVgpl40.mut8.modSF162delV1V2	5133	27 Dec 99
	pCMVKm2.Gagprot.Mod.SF2.GP1	5150	27 Dec 99
20	pCMVKm2.Gagprot.Mod.SF2.GP2	5151	27 Dec 99

Example 2

Expression Assays for the Synthetic Gag, Env and Tat Coding Sequences

25 A. Gag and Gag-Protease Coding Sequences

The HIV-1SF2 wild-type Gag (SEQ ID NO:1) and Gag-protease (SEQ ID NO:2) sequences were cloned into expression vectors having the same features as the vectors into which the synthetic Gag (SEQ ID NO:4) and
30 Gag-protease (SEQ ID NOs:5, 78 or 79)) sequences were cloned.

Expression efficiencies for various vectors carrying the HIV-1SF2 wild-type and synthetic Gag sequences were evaluated as follows. Cells from several mammalian cell lines (293, RD, COS-7, and CHO; all obtained from the American Type Culture Collection, 10801 University Boulevard, Manassas, VA 20110-2209) were transfected with 2 μ g of DNA in transfection reagent LT1 (PanVera Corporation, 545 Science Dr., Madison, WI). The cells were incubated for 5 hours in reduced serum medium (Opti-MEM, Gibco-BRL, Gaithersburg, MD). The medium was then replaced with normal medium as follows: 293 cells, IMDM, 10% fetal calf serum, 2% glutamine (BioWhittaker, Walkersville, MD); RD and COS-7 cells, D-MEM, 10% fetal calf serum, 2% glutamine (Opti-MEM, Gibco-BRL, Gaithersburg, MD); and CHO cells, Ham's F-12, 10% fetal calf serum, 2% glutamine (Opti-MEM, Gibco-BRL, Gaithersburg, MD). The cells were incubated for either 48 or 60 hours. Supernatants were harvested and filtered through 0.45 μ m syringe filters and, optionally, stored at -20°C.

Supernatants were evaluated using the Coulter p24-assay (Coulter Corporation, Hialeah, FL, US), using 96-well plates coated with a murine monoclonal antibody directed against HIV core antigen. The HIV-1 p24 antigen binds to the coated wells. Biotinylated antibodies against HIV recognize the bound p24 antigen. Conjugated streptavidin-horseradish peroxidase reacts with the biotin. Color develops from the reaction of peroxidase with TMB substrate. The reaction is terminated by addition of 4N H₂SO₄. The intensity of the color is directly proportional to the amount of HIV p24 antigen in a sample.

The results of these expression assays are presented in Tables 2A and 2B. Tables 2A and 2B shows data

obtained using the synthetic Gag-protease expression cassette of SEQ ID NO:5. Similar results were obtained using the Gag-protease expression cassettes of SEQ ID NOs:78 and 79.

5

Table 2: in vitro gag and gagprot p24 expression

5 TABLE 2a. Increased in vitro expression from modified vs. native *gag* plasmids in supernatants and lysates from transiently transfected cells

experiment	native (nat) ^a modified (mod) ^b	supernatant (sup) lysate (lys)	cell line	hours post transfection	total ng p24 (fold increase)
1	nat	sup	293	48	3.4
	mod	sup	293	48	1260 (371)
	nat	sup	293	60	3.2
	mod	sup	293	60	2222 (694)
2	nat	sup	293	60	1.8
	mod	sup	293	60	1740 (966)
3	nat	sup	293	60	1.8
	mod	sup	293	60	580 (322)
4	nat	lys	293	60	1.5
	mod	lys	293	60	85 (57)
1	nat	sup	RD	48	5.6
	mod	sup	RD	48	66 (12)
	nat	sup	RD	60	7.8
	mod	sup	RD	60	70.2 (9)
2	nat	lys	RD	60	1.9
	mod	lys	RD	60	7.8 (4)
1	nat	sup	COS-7	48	0.4
	mod	sup	COS-7	48	33.4 (84)
2	nat	sup	COS-7	48	0.4
	mod	sup	COS-7	48	10 (25)
	nat	lys	COS-7	48	3
	mod	lys	COS-7	48	14 (5)

^a pCMVLink.Gag.SF2.PRE

^b pCMVKm2.GagMod.SF2

5 TABLE 2b. *In vitro* expression from modified *gag* and *gagprotease* plasmids in supernatants and lysates from transiently transfected cells

plasmid	supernatant (sup) lysate (lys)	cell line	hours post transfection	total ng p24 ^d
Gag ^a	sup	293	60	760
GagProt(GP1) ^b	sup	293	60	380
GagProt(GP2) ^c	sup	293	60	320
Gag	lys	293	60	78
GagProt(GP1)	lys	293	60	1250
GagProt(GP2)	lys	293	60	400
Gag	sup	COS-7	72	40
GagProt(GP1)	sup	COS-7	72	150
GagProt(GP2)	sup	COS-7	72	290
Gag	lys	COS-7	72	60
GagProt(GP1)	lys	COS-7	72	63
GagProt(GP2)	lys	COS-7	72	58

^a pCMVKm2.GagMod.SF2

^b pCMVKm2.GagProtMod.SF2(GP1) *gagprotease* with codon optimization and inactivation of INS in *protease*

^c pCMVKm2.GagProtMod.SF2(GP2) *gagprotease* with only inactivation of INS in *protease*

^d Shown are representative results from 3 independent experiments for each cell line tested.

The data showed that the synthetic Gag and Gag-protease expression cassettes provided dramatic increases in production of their protein products, relative to the native (HIV-1SF2 wild-type) sequences, when expressed in a variety of cell lines.

B. Env Coding Sequences

The HIV-SF162 ("SF162") wild-type Env (SEQ ID NO:1-3) and HIV-US4 ("US4") wild-type Env (SEQ ID NO:22-24) sequences were cloned into expression vectors having the same features as the vectors into which the synthetic Env sequences were cloned.

Expression efficiencies for various vectors carrying the SF162 and US4 wild-type and synthetic Env sequences were evaluated essentially as described above for Gag except that cell lysates were prepared in 40 μ l lysis buffer (1.0 % NP40, 0.1 M Tris pH 7.5) and frozen at -20°C and capture ELISAs were performed as follows.

For Capture ELISAs, 250 ng of an ammonium sulfate IgG cut of goat polyclonal antibody to gp120SF2/env2-3 was used to coat each well of a 96-well plate (Corning, Corning, NY). Serial dilutions of gp120/SF2 protein (MID 167) were used to set the quantitation curve from which expression of US4 or SF162 gp120 proteins from transfection supernatant and lysates were calculated. Samples were screened undiluted and, optionally, by serial 2-fold dilutions. A human polyclonal antibody to HIV-1 gp120/SF2 was used to detect bound gp120 envelope protein, followed by horse-radish peroxidase (HRP)-labeled goat anti-human IgG conjugates. TMB (Pierce, Rockford, IL) was used as the substrate and the reaction is terminated by addition of 4N H₂SO₄. The reaction was quantified by measuring the optical density (OD) at 450 nm. The intensity of the color is directly

proportional to the amount of HIV gp120 antigen in a sample. Purified SF2 gp120 protein was diluted and used as a standard.

5 The results of the transient expression assays are presented in Tables 3 and 4. Table 3 depicts transient expression in 293 cells transfected with a pCMVKm2 vector carrying the Env cassette of interest. Table 4 depicts transient expression in RD cells transfected with a pCMVKm2 vector carrying the Env cassette of interest.

5

Table 3

Native (N) Synthetic (S)	Cell Line	Total sup (ng)	Sup fold increase (S v. N)	Total cell lysate (ng)	Cell lysate fold increase (S v. N)	Total (ng)	Total fold increase (S v. N)
N-gp120.US4	RD	87		<1		88	
S-gp120.modUS4	RD	690	8	2	5	693	8
N-gp140.US4	RD	526		0		526	
S-gp140.modUS4	RD	1305	2	1	2	1306	2
S-gp140mut.modUS4	RD	35	N/A	25	N/A	60	N/A
S-gp140TM.modUS4	RD	0	N/A	5	N/A	5	N/A
N-gp160.US4	RD	0		8		8	
S-gp160.modUS4	RD	0	0	30	4	30	4

Table 4

CHO Cell Lines Expression Level of US4 Envelope Constructs			
Constructs	CHO Clone #	MTX Level	Expression Level* (ng/ml)
gp120.modUS4	1	3.2 μ M	250-450
	2	1.6 μ M	350-450
	3	200nM	230-580
	4	200nM	300-500
gp140.modUS4	1	1 μ M	155-300
	2	1 μ M	100-260
	3	1 μ M	200-430
gp140.mut. modUS4	1	1 μ M	110-270
	2	1 μ M	100-235
	3	1 μ M	100-220
gp140.modUS4 .delV1/V2	1	50nM	313-587**
	2	50nM	237-667**
	3	50nM	492-527**
gp140.mut. modUS4.delV1 /V2	1	50nM	46-328**
	2	50nM	82-318**
	3	50nM	204-385**

*All samples measured at T-75 flask stage unless otherwise indicated

**at 24 well and 6 well plate stages

***in a three liter bioreactor perfusion culture this clone yielded approximately 2-5 μ g/ml.

The data showed that the synthetic Env and expression cassettes provided a significant increase in production of their protein products, relative to the native (HIV-1SF162 or US4 wild-type) sequences, when
5 expressed in a variety of cell lines.

C. CHO Cell line Env expression data

Chinese hamster ovary (CHO) cells were transfected with plasmid DNA encoding the synthetic HIV-1 gp120 or
10 gp140 proteins (e.g., pESN2dhfr or pCMVIII vector backbone) using Mirus TransIT-LT1 polyamine transfection reagent (Pan Vera) according to the manufacturers instructions and incubated for 96 hours. After 96 hours, media was changed to selective media (F12 special with
15 250 μ g/ml G418) and cells were split 1:5 and incubated for an additional 48 hours. Media was changed every 5-7 days until colonies started forming at which time the colonies were picked, plated into 96 well plates and screened by gp120 Capture ELISA. Positive clones were
20 expanded in 24 well plates and screened several times for Env protein production by Capture ELISA, as described above. After reaching confluency in 24 well plates, positive clones were expanded to T25 flasks (Corning, Corning, NY). These were screened several times after
25 confluency and positive clones were expanded to T75 flasks.

Positive T75 clones were frozen in LN2 and the highest expressing clones amplified with 0-5 μ M methotrexate (MTX) at several concentrations and plated in
30 100mm culture dishes. Plates were screened for colony formation and all positive clones were again expanded as described above. Clones were expanded and amplified and screened at each step by gp120 capture ELISA. Positive clones were frozen at each methotrexate level. Highest

producing clones were grown in perfusion bioreactors (3L, 100L) for expansion and adaptation to low serum suspension culture conditions for scale-up to larger bioreactors.

5 Tables 5 and 6 show Capture ELISA data from CHO cells transfected with pCMVIII vector carrying a cassette encoding synthetic HIV-US4 and SF162 Env polypeptides (e.g., mutated cleavage sites, modified codon usage and/or deleted hypervariable regions). Thus, stably
10 transfected CHO cell lines which express Env polypeptides (e.g., gp120, gp140-monomeric, and gp140-oligomeric) have been produced.

Table 5

CHO Cell Lines Expression Level of US4 Envelope Constructs			
Constructs	CHO Clone #	MTX Level	Expression Level* (ng/ml)
gp120.modUS4	1	3.2 μ M	250-450
	2	1.6 μ M	350-450
	3	200nM	230-580***
	4	200nM	300-500
gp140.modUS4	1	1 μ M	155-300
	2	1 μ M	100-260
	3	1 μ M	200-430
gp140.mut. modUS4	1	1 μ M	110-270
	2	1 μ M	100-235
	3	1 μ M	100-220
gp140.modUS4 .delV1/V2	1	50nM	313-587**
	2	50nM	237-667**
	3	50nM	492-527**
gp140.mut. modUS4.delV1 /V2	1	50nM	46-328**
	2	50nM	82-318**
	3	50nM	204-385**

*All samples measured at T-75 flask stage unless otherwise indicated

**at 24 well and 6 well plate stages

***in a three liter bioreactor perfusion culture this clone yielded approximately 2-5 μ g/ml.

Table 6

CHO Cell Lines Expression Level of SF162 Envelope Constructs			
Constructs	CHO Clone #	MTX Level	Expression Level* (ng/ml)
gp120.modSF162	1	0	755-2705
	2	0	928-1538
	3	0	538-1609
gp140.modSF162	1	20 nM	180-350
gp140.mut. modSF162	1	20 nM	164-451
	2	20 nM	188-487
	3	20 nM	233-804
gp120.modSF162 .delV2	1	800nM	528-1560
	2	800nM	487-1878
	3	800nM	589-1212
gp140.modSF162 .delV2	1	800nM	300-600
	2	800nM	200-400
	3	800nM	200-500
gp140.mut. modSF162.delV2	1	800nM	300-700
	2	400nM	1161
	3	800nM	400-600
	4	400nM	1600-2176

*All samples measured at T-75 flask stage unless otherwise indicated

The results presented above demonstrate the ability of the constructs of the present invention to provide expression of Env polypeptides in CHO cells. Production of polypeptides using CHO cells provides (i) correct glycosylation patterns and protein conformation (as determined by binding to panel of MAbs); (ii) correct binding to CD4 receptor molecules; (iii) absence of non-

mammalian cell contaminants (e.g., insect viruses and/or cells); and (iv) ease of purification.

D. Tat Coding Sequences

5 The HIV-SF162 ("SF162") wild-type Tat (SEQ ID NO:85) sequences were cloned into expression vectors having the same features as the vectors into which the synthetic Tat sequences were cloned (SEQ ID NOs:87, 88 and 89).

10 Expression efficiencies for various vectors carrying the SF162 wild-type and synthetic Tat sequences are evaluated essentially as described above for Gag and Env using capture ELISAs with the appropriate anti-tat antibodies and/or CHO cell assays. Expression of the polypeptides encoded by the synthetic cassettes is
15 improved relative to wild type.

Example 3

Western Blot Analysis of Expression

A. Gag and Gag-Protease Coding Sequences

20 Human 293 cells were transfected as described in Example 2 with pCMV6a-based vectors containing native or synthetic Gag expression cassettes. Cells were cultivated for 60 hours post-transfection. Supernatants were prepared as described. Cell lysates were prepared
25 as follows. The cells were washed once with phosphate-buffered saline, lysed with detergent [1% NP40 (Sigma Chemical Co., St. Louis, MO) in 0.1 M Tris-HCl, pH 7.5], and the lysate transferred into fresh tubes. SDS-polyacrylamide gels (pre-cast 8-16%; Novex, San Diego,
30 CA) were loaded with 20 μ l of supernatant or 12.5 μ l of cell lysate. A protein standard was also loaded (5 μ l, broad size range standard; BioRad Laboratories, Hercules, CA). Electrophoresis was carried out and the proteins were transferred using a BioRad Transfer Chamber (BioRad

Laboratories, Hercules, CA) to Immobilon P membranes (Millipore Corp., Bedford, MA) using the transfer buffer recommended by the manufacturer (Millipore), where the transfer was performed at 100 volts for 90 minutes. The
5 membranes were exposed to HIV-1-positive human patient serum and immunostained using o-phenylenediamine dihydrochloride (OPD; Sigma).

The results of the immunoblotting analysis showed that cells containing the synthetic Gag expression
10 cassette produced the expected p55 protein at higher per-cell concentrations than cells containing the native expression cassette. The Gag p55 protein was seen in both cell lysates and supernatants. The levels of production were significantly higher in cell supernatants
15 for cells transfected with the synthetic Gag expression cassette of the present invention. Experiments performed in support of the present invention suggest that cells containing the synthetic Gag-prot expression cassette produced the expected Gag-prot protein at comparably
20 higher per-cell concentrations than cells containing the native expression cassette.

In addition, supernatants from the transfected 293 cells were fractionated on sucrose gradients. Aliquots of the supernatant were transferred to Polyclear™ ultra-
25 centrifuge tubes (Beckman Instruments, Columbia, MD), under-laid with a solution of 20% (wt/wt) sucrose, and subjected to 2 hours centrifugation at 28,000 rpm in a Beckman SW28 rotor. The resulting pellet was suspended in PBS and layered onto a 20-60% (wt/wt) sucrose gradient
30 and subjected to 2 hours centrifugation at 40,000 rpm in a Beckman SW41ti rotor.

The gradient was then fractionated into approximately 10 x 1 ml aliquots (starting at the top, 20%-end, of the gradient). Samples were taken from

fractions 1-9 and were electrophoresed on 8-16% SDS polyacrylamide gels. Fraction number 4 (the peak fraction) corresponds to the expected density of Gag protein VLPs. The supernatants from 293/synthetic Gag cells gave much stronger p55 bands than supernatants from 293/native Gag cells, and, as expected, the highest concentration of p55 in either supernatant was found in fraction 4.

These results demonstrate that the synthetic Gag expression cassette provides superior production of both p55 protein and VLPs, relative to the native Gag coding sequences.

B. Env Coding Sequences

Human 293 cells were transfected as described in Example 2 with pCMVKm2-based; pCMVlink-based; p-CMVII-based or pESN2-based vectors containing native or synthetic Env expression cassettes. Cells were cultivated for 48 or 60 hours post-transfection. Cell lysates and supernatants were prepared as described (Example 2). Briefly, the cells were washed once with phosphate-buffered saline, lysed with detergent [1% NP40 (Sigma Chemical Co., St. Louis, MO)] in 0.1 M Tris-HCl, pH 7.5], and the lysate transferred into fresh tubes. SDS-polyacrylamide gels (pre-cast 8-16%; Novex, San Diego, CA) were loaded with 20 μ l of supernatant or 12.5 μ l of cell lysate. A protein molecular weight standard and an HIV SF2 gp120 positive control protein (5 μ l, broad size range standard; BioRad Laboratories, Hercules, CA) were also loaded. Electrophoresis was carried out and the proteins were transferred using a BioRad Transfer Chamber (BioRad Laboratories, Hercules, CA) to Immobilon P membranes (Millipore Corp., Bedford, MA) using the transfer buffer recommended by the manufacturer

(Millipore), where the transfer was performed at 100 volts for 90 minutes. The membranes were then reacted against polyclonal goat anti-gp120SF2/env2-3 anti-sera, followed by incubation with swine anti-goat IgG-
5 peroxidase (POD) (Sigma, St. Louis, MO). Bands indicative of binding were visualized by adding DAB with hydrogen peroxide which deposits a brown precipitate on the membranes.

The results of the immunoblotting analysis showed
10 that cells containing the synthetic Env expression cassette produced the expected Env gp proteins of the predicted molecular weights as determined by mobilities in SDS-polyacrylamide gels at higher per-cell concentrations than cells containing the native
15 expression cassette. The Env proteins were seen in both cell lysates and supernatants. The levels of production were significantly higher in cell supernatants for cells transfected with the synthetic Env expression cassette of the present invention.

20 C. Tat Coding Sequences

Human 293 cells are transfected as described in Example 2 with various vectors containing native or synthetic Tat expression cassettes. Cells are cultivated
25 and isolated proteins analyzed as described above. Immunoblotting analysis shows that cells containing the synthetic Tat expression cassette produced the expected Tat proteins of the predicted molecular weights as determined by mobilities in SDS-polyacrylamide gels at
30 higher per-cell concentrations than cells containing the native expression cassette.

Example 4

Purification of Env polypeptides

A. Purification of Oligomeric gp140

Purification of oligomeric gp140 (o-gp140 US4) was
5 conducted essentially as shown in Figure 60. For the
experiments described herein, o-gp140 refers to
oligomeric gp140 in either native or modified (e.g.,
optimized expression sequences, deleted, mutated,
truncated, etc.) form. Briefly, concentrated (30-50X)
10 supernatants obtained from CHO cell cultures were loaded
onto an anion exchange (DEAE) column which removed DNA
and other serum proteins. The eluted material was loaded
onto a ceramic hydroxyapatite column (CHAP) which bound
serum proteins but not HIV Env proteins. The flow-
15 through from the DEAE and CHAP columns was loaded onto a
Protein A column as a precautionary step to remove any
remaining serum immunoglobulins. The Env proteins in the
flow-through were then captured using the lectin
gluconanthus navalis (GNA, Vector Labs, Burlingame, CA).
20 GNA has high affinity for mannose rich carbohydrates such
as Env. The Env proteins were then eluted with GNA
substrate. To remove other highly glycosylated proteins,
a cation exchange column (SP) was used to purify
gp140/gp120. In a final step, which separates gp120 from
25 o-gp140, a gel filtration column was used to separate
oligomers from monomers. Sizing and chromatography
analysis of the final product revealed that this strategy
lead to the successful isolation of oligomeric gp140.

B. Purification of gp120

Purification of gp120 was conducted essentially as
previously described for other Env proteins. Briefly,
concentrated supernatants obtained from CHO cell cultures
were loaded onto an anion exchange (DEAE) column which

removed DNA and other serum proteins. The eluted material was loaded onto a ceramic hydroxyapatite column (CHAP) which bound serum proteins but not HIV Env proteins. The flow-through from the CHAP column was
5 loaded a cation exchange column (SP) where the flow-through was discarded and the bound fraction eluted with salt. The eluted fraction(s) were loaded onto a Suprose 12/Superdex 200 Tandem column (Pharmacia-Upjohn, Uppsala, Sweden) from which purified gp120 was obtained. Sizing
10 and chromatography analysis of the final product revealed that this strategy successfully purified gp120 proteins.

Example 5

Analysis of Purified Env Polypeptides

15 A. Analysis of o-gp140

It is well documented that HIV Env protein binds to CD4 only in its correct conformation. Accordingly, the ability of o-gp140 US4 polypeptides, produced and purified as described above, to bind CD4 cells was
20 tested. O-gp140 US4 was incubated for 15 minutes with FITC-labeled CD4 at room temperature and loaded onto a Biosil 250 (BioRad) size exclusion column using Waters HPLC. CD4-FITC has the longest retention time (2.67 minutes), followed by CD4-FITC-gp120 (2.167 min). The
25 shortest retention time (1.9 min) was observed for CD4-FITC-o-gp140 US4 indicating that, as expected, o-gp140 US4 binds to CD4 forming a large complex which reduces retention time on the column. Thus, the o-gp140 US4 produced and purified as described above is of the
30 correct size and conformation.

In addition, the US4 o-gp140, purified as described above, was also tested for its ability to bind to a variety of monoclonal antibodies with known epitope specificities for the CD4 binding site, the CD4 inducible

site, the V3 loop and oligomer-specific gp41 epitope. O-gp140 bound strongly to these antibodies, indicating that the purified protein retains its structural integrity.

5 B. Analysis of gp120

As described above, CD4-FITC binds gp120, as demonstrated by the decreased retention time on the HPLC column. Thus, US4 gp120 purified by the above method retains its conformational integrity. In addition, the
10 properties of purified gp120 can be tested by examining its integrity and identity on western blots, as well as, by examining protein concentration, pH, conductivity, endotoxin levels, bioburden and the like. US4 gp120, purified as described above, was also tested for its
15 ability to bind to a variety of monoclonal antibodies with known epitope specificities for the CD4 binding site, the CD4 inducible site, the V3 loop and oligomer-specific gp41 epitope. The pattern of mAb binding to gp120 indicated that the purified protein retained its
20 structural integrity, for example, the purified gp120 did not bind the mAb having the oligomer-specific gp41 epitope (as expected).

Example 6

25 Electron Microscopic Evaluation of VLP Production

The cells for electron microscopy were plated at a density of 50-70% confluence, one day before transfection. The cells were transfected with 10 µg of DNA using transfection reagent LT1 (Panvera) and
30 incubated for 5 hours in serum-reduced medium (see Example 2). The medium was then replaced with normal medium (see Example 2) and the cells were incubated for 14 hours (COS-7) or 40 hours (CHO). After incubation the cells were washed twice with PBS and fixed with 2%

glutaraldehyde. Electron microscopy was performed by Prof. T.S. Benedict Yen, Veterans Affairs, Medical Center, San Francisco, CA).

Electron microscopy was carried out using a transmission electron microscope (Zeiss 10c). The cells were pre-stained with osmium and stained with uranium acetate and lead citrate. The magnification was 100,000X.

Figures 3A and 3B show micrographs of CHO cells transfected with pCMVKM2 carrying the synthetic Gag expression cassette (SEQ ID NO:5) or carrying the Gag-prot expression cassette (SEQ ID NO:79). In the figure, free and budding immature virus-like-particles (VLP) of the expected size (100 nm) are seen for the Gag expression cassette (Figure 3A) and both immature and mature VLPs are seen for the Gag-prot expression cassette (Figure 3B). COS-7 cells transfected with the same vector have the same expression pattern. VLP can also be found intracellularly in CHO and COS-7 cells.

Native and synthetic Gag expression cassettes were compared for their associated levels of VLP production when used to transfect human 293 cells. The comparison was performed by density gradient ultracentrifugation of cell supernatants and Western-blot analysis of the gradient fractions. There was a clear improvement in production of VLPs when using the synthetic Gag construct.

Example 7

Expression of Virus-like Particles in the Baculovirus System

A. Expression of Native HIV p55 Gag

To construct the native HIV p55 Gag baculovirus shuttle vector, the prototype SF2 HIV p55 plasmid, pTM1-

Gag (Selby M.J., et al., *J Virol.* 71(10):7827-7831, 1997), was digested with restriction endonucleases *Nco*I and *Bam*HI to extract a 1.5 Kb fragment that was subsequently subcloned into pAcC4 (*Bio/Technology* 6:47-55, 1988), a derivative of pAc436. Generation of the recombinant baculovirus was achieved by co-transfecting 2 μ g of the HIV p55 Gag pAcC4 shuttle vector with 0.5 μ g of linearized, *Autographa californica* baculovirus (AcNPV) wild-type viral DNA into *Spodoptera frugiperda* (Sf9) cells (Kitts, P.A., Ayres M.D., and Possee R.D., *Nucleic Acids Res.* 18:5667-5672, 1990). The isolation of recombinant virus expressing HIV p55 Gag was performed according to standard techniques (O'Reilly, D.R., L.K. Miller, and V. A. Luckow, *Baculovirus Expression Vector: A Laboratory Manual*, W.H. Freeman and Company, New York, 1992).

Expression of the HIV p55 Gag was achieved using a 500 ml suspension culture of Sf9 cells grown in serum-free medium (Miaorella, B., D. Inlow, A. Shauger, and D. Harano, *Bio/Technology* 6:1506-1510, 1988) that had been infected with the HIV p55 Gag recombinant baculovirus at a multiplicity of infection (MOI) of 10. Forty-eight hours post-infection, the supernatant was separated by centrifugation and filtered through a 0.2 μ m filter. Aliquots of the supernatant were then transferred to Polyclear™ (Beckman Instruments, Palo Alto, CA) ultracentrifuge tubes, underlaid with 20% (wt/wt) sucrose, and subjected to 2 hours centrifugation at 24,000 rpm using a Beckman SW28 rotor.

The resulting pellet was suspended in Tris buffer (20 mM Tris HCl, pH 7.5, 250 mM NaCl, and 2.5 mM ethylenediaminetetraacetic acid [EDTA]), layered onto a 20-60% (wt/wt) sucrose gradient, and subjected to 2 hours centrifugation at 40,000 rpm using a Beckman SW41ti

rotor. The gradient was then fractionated starting at the top (20% sucrose) of the gradient into approximately twelve 0.75 ml aliquots. A sample of each fraction was electrophoresed on 8-16% SDS polyacrylamide gels and the resulting bands were visualized after commassie staining (Figure 4). Additional aliquots were subjected to refractive index analysis.

The results shown in Figure 4 indicated that the p55 Gag virus-like particles banded at a sucrose density of range of 1.15 - 1.19 g/ml with the peak at approximately 1.17 g/ml. The peak fractions were pooled and concentrated by a second 20% sucrose pelleting. The resulting pellet was suspended in 1 ml of Tris buffer (described above). The total protein yield as estimated by Bicimchrominic Acid (BCA) (Pierce Chemical, Rockford, IL) was 1.6 mg.

B. Expression of Synthetic HIV p55 Gag

A baculovirus shuttle vector containing the synthetic p55 Gag sequence was constructed as follows. The synthetic HIV p55 expression cassette (Example 1) was digested with restriction enzyme *SalI* followed by incubation with T4-DNA polymerase. The resulting fragment was isolated (PCR Clean-Up™, Promega, Madison, WI) and then digested with *BamHI* endonuclease. The shuttle vector pAcC13 (Munemitsu S., et al., *Mol Cell Biol.* 10(11):5977-5982, 1990) was linearized by digestion with *EcoI*, followed by incubation with T4-DNA polymerase, and then isolated (PCR Clean-Up™). The linearized vector was digested with *BamHI*, treated with alkaline phosphatase, and isolated by size fragmentation in an agarose gel. The isolated 1.5 kb fragment was ligated with the prepared pAcC13 vector. The resulting clone was designated pAcC13-Modif.p55Gag.

The expression conditions for the synthetic HIV p55 VLPs differed from those of the native p55 Gag as follows: a culture volume of 1 liter used instead of 500 ml; *Trichoplusia ni* (Tn5) (Wickham, T.J., and Nermerow, G.R., *BioTechnology Progress*, 9:25-30, 1993) insect cells were used instead of Sf9 insect cells; and, an MOI of 3 was instead of an MOI of 10. Experiments performed in support of the present invention showed that there was no appreciable difference in expression level between the Sf9 and Tn5 insect cells with the native p55 clone. In terms of MOI, experience with the native p55 clone suggested that an MOI of 10 resulted in higher expression (approximately 2-fold) of VLPs than a lower MOI.

The sucrose pelleting and banding methods used for the synthetic p55 VLPs were similar to those employed for the native p55 VLPs (described above), with the following exceptions: pelleted VLPs were suspended in 4 ml of phosphate buffered saline (PBS) instead of 1.0 ml of the Tris buffer; and four, 20-60% sucrose gradients were used instead of a single gradient. Also, due to the high concentration of banded VLPs, further concentration by pelleting was not required. The peak fractions from all 4 gradients were simply dialyzed against PBS. The approximate density of the banded VLPs ranged from 1.23-1.28 g/ml. A total protein yield as estimated by BCA was 46 mg. Results from the sucrose gradient banding of the synthetic p55 are shown in Figure 5.

A comparison of the total amount of purified HIV p55 Gag from several preparations obtained from the two baculovirus expression cassettes has been summarized in Figure 6. The average yield from the native p55 was 3.16 mg/liter of culture (n=5, standard deviation (sd) ± 1.07 , range = 1.8-4.8 mg/L) whereas the average yield from the

synthetic p55 was more than ten-fold higher at 44.5 mg/liter of culture (n=2, sd=±6.4).

In addition to a higher total protein yield, the final product from the synthetic p55-expressed Gag consistently contained lower amounts of contaminating baculovirus proteins than the final product from the native p55-expressed Gag. This difference can be seen in the two commassie-stained gels Figures 4 and 5.

10 C. Expression of Native and Synthetic Gag-Core

Expression of the HIV p55 Gag/HCV Core 173 (SEQ ID NO:8) was achieved using a 2.5 liter suspension culture of Sf9 cells grown in serum-free medium (Miaorella, B., D. Inlow, A. Shauger, and D. Harano. 1988 Bio/Technology 6:1506-1510). The cells were infected with an HIV p55 Gag/HCV Core 173 recombinant baculovirus. Forty-eight hours post-infection, the supernatant was separated from the cells by centrifugation and filtered through a 0.2 μ m filter. Aliquots of the supernatant were then

20 transferred to a Polyclear™ (Beckman Instruments, Palo Alto, CA) ultracentrifuge tubes containing 30% (wt/wt) sucrose, and subjected to 2 hours of centrifugation at 24,000 rpm in a Beckman SW28 rotor and ultracentrifuge.

The resulting pellet was suspended in Tris buffer (50 mM Tris-HCl, pH 7.5, 500 mM NaCl) and layered onto a 30-60% (wt/wt) sucrose gradient and subjected to 2 hours centrifugation at 40,000 rpm in a Beckman SW41ti rotor and ultracentrifuge. The gradient was then fractionated starting at the top (30%) of the gradient into approximately 11 x 1.0 ml aliquots. A sample of each fraction was electrophoresed on 8-16% SDS polyacrylamide gels and the resulting bands were visualized after commassie staining.

A subset of aliquots were also subjected to Western blot analysis using monoclonal antibody 76C.5EG (Steimer, K.S., et al., *Virology* 150:283-290, 1986) which is specific for HIV p24 (a subunit of HIV p55). The peak fractions from the sucrose gradient were pooled and concentrated by a second 20% sucrose pelleting. The resulting pellet was suspended in 1 ml of buffer Tris buffer and the total protein yield as estimated by BCA (Pierce Chemical, Rockford, IL) was ~ 1.0 mg.

The results from the SDS PAGE are shown in Figure 8 and the anti- p24 Western blot results are shown in Figure 9. Taken together, these results indicate that the HIV p55 Gag/HCV Core 173 chimeric VLPs banded at a sucrose density similar to that of the HIV p55 Gag VLPs and the visible protein band that migrated at a molecular weight of ~ 72,000 kd was reactive with the HIV p24-specific monoclonal antibody. An additional immunoreactive band at approximately 55,000 kd also appeared to be reactive with the anti-p24 antibody and may be a degradation product.

Although aliquots from the above preparation were not tested for reactivity with an HCV Core-specific antibody (an anti-CD22 rabbit serum), results from a similar preparation are shown in Figure 10 and indicate that the main HCV Core-specific reactivity migrates at an approximate molecular weight of 72,000 kd which is in accordance with the predicted molecular weight of the chimeric protein.

The expression conditions for the synthetic HIV p55 Gag/HCV Core 173 (SEQ ID NO:8) VLPs differed from those of the native p55 Gag and are as follows: a culture volume of 1 liter used instead of 2.5 liters, *Trichoplusia ni* (Tn5) (Wickham, T.J., and Nemerow, G.R. 1993 *BioTechnology Progress*, 9:25-30) insect cells were

used instead of Sf9 insect cells and an MOI of 3 was instead of an MOI of 10. The sucrose pelleting and banding methods used for the synthetic HIV p55 Gag/HCV Core 173 VLPs were similar to those employed for the native HIV p55 Gag/HCV Core 173 VLPs. However, differences included: pelleted VLPs were suspended in 1 ml of phosphate buffered saline (PBS) instead of 1.0 ml of the Tris buffer, and a single 20-60% sucrose gradients was used. A comparison of the total amount of purified HIV p55 Gag/HCV Core 173 from multiple preparations obtained from the two baculovirus expression cassettes showed that there was an increase in expression using the synthetic HIV p55 Gag/HCV Core 173 cassette.

D. Alternative method for the enrichment of HIV p55 Gag VLPs

In addition to purification from the media, p55 (Gag protein) expressed in baculovirus (e.g., using a synthetic expression cassette of the present invention) can also be purified as virus-like particles from the infected insect cells. For example, forty-eight hours post infection, the media and cell pellet are separated by centrifugation and the cell pellet is stored at -70°C until future use. At the time of processing, the cell pellet is suspended in 5 volumes of hypotonic lysis buffer (20 mM Tris-HCl, pH 8.2, 1 mM EGTA; 1 mM MgCl₂, and Complete Protease Inhibitor® (Boehringer Mannheim Corp., Indianapolis, IN)). If needed, the cells are then dounced 8-10 times to complete cell lysis.

The lysate is then centrifuged at approximately 1000-1500 x g for 20 minutes. The supernatant is

decanted into UltraClear™ tubes, underlayered with 20% sucrose (w/w) and centrifuged at 24,000 rpm in SW28 buckets for 2 hours. The resulting pellet is suspended in Tris buffer (20 mM Tris HCl, pH 7.5, 250 mM NaCl, and 2.5 mM ethylenediamine-tetraacetic acid (EDTA) with 0.1% IGEPAL detergent (Sigma Chemical, St. Louis, MO) and 250 units/ml of benzonase (American International Chemical, Inc., Natick, MA) and incubated at 4°C for at least 30 minutes. The suspension is subsequently layered onto a 20-60% sucrose gradient and spun at 40,000 rpm using an SW41ti rotor for 20-24 hours.

After ultracentrifugation, the sucrose gradient is fractionated and aliquots run on SDS PAGE to identify peak fractions. The peak fractions are dialyzed against PBS and measured for protein content. Negatively stained electron micrographs typically show non-enveloped VLPs somewhat smaller in diameter (80-120 nm) than the budded VLPs. HIV Gag VLPs prepared in this manner are also capable of generating Gag-specific CTL responses in mice.

Example 8

In Vivo Immunogenicity of Synthetic Gag Expression Cassettes

A. Immunization

To evaluate the possibly improved immunogenicity of the synthetic Gag expression cassettes, a mouse study was performed. The plasmid DNA, pCMVKM2 carrying the synthetic Gag expression cassette, was diluted to the following final concentrations in a total injection volume of 100 µl: 20 µg, 2 µg, 0.2 µg, and 0.02 µg. To

overcome possible negative dilution effects of the diluted DNA, the total DNA concentration in each sample was brought up to 20 μ g using the vector (pCMVKM2) alone. As a control, plasmid DNA of the native Gag expression cassette was handled in the same manner. Twelve groups of four Balb/c mice (Charles River, Boston, MA) were intramuscularly immunized (50 μ l per leg, intramuscular injection into the *tibialis anterior*) according to the schedule in Table 7.

Table 7

Group	Gag Expression Cassette	Concentration of Gag plasmid DNA (μ g)	Immunized at time (weeks):
1	Synthetic	20	0 ¹ , 4
2	Synthetic	2	0, 4
3	Synthetic	0.2	0, 4
4	Synthetic	0.02	0, 4
5	Synthetic	20	0
6	Synthetic	2	0
7	Synthetic	0.2	0
8	Synthetic	0.02	0
9	Native	20	0
10	Native	2	0
11	Native	0.2	0
12	Native	0.02	0

1 = initial immunization at "week 0"

Groups 1-4 were bled at week 0 (before immunization), week 4, week 6, week 8, and week 12. Groups 5-12 were bled at week 0 (before immunization) and at week 4.

B. Humoral Immune Response

The humoral immune response was checked with an anti-HIV Gag antibody ELISAs (enzyme-linked immunosorbent assays) of the mice sera 0 and 4 weeks post immunization (groups 5-12) and, in addition, 6 and 8 weeks post immunization, respectively, 2 and 4 weeks post second immunization (groups 1-4).

The antibody titers of the sera were determined by anti-Gag antibody ELISA. Briefly, sera from immunized mice were screened for antibodies directed against the HIV p55 Gag protein. ELISA microtiter plates were coated with 0.2 μ g of HIV-1_{SP2} p24-Gag protein per well overnight and washed four times; subsequently, blocking was done with PBS-0.2% Tween (Sigma) for 2 hours. After removal of the blocking solution, 100 μ l of diluted mouse serum was added. Sera were tested at 1/25 dilutions and by serial 3-fold dilutions, thereafter. Microtiter plates were washed four times and incubated with a secondary, peroxidase-coupled anti-mouse IgG antibody (Pierce, Rockford, IL). ELISA plates were washed and 100 μ l of 3, 3', 5, 5'-tetramethyl benzidine (TMB; Pierce) was added per well. The optical density of each well was measured after 15 minutes. The titers reported are the reciprocal of the dilution of serum that gave a half-maximum optical density (O.D.). The ELISA results are presented in Table 8.

Table 8

Group	Inoculum (μ g)	Expression cassette	Sera - Week 4 ³	Sera - Week 6	Sera - Week 8
1	20	S ¹ - gag	98	455	551
2	2	S - gag	59	1408	227
3	0.	S - gag	29	186	61
4	0.02	S - gag	< 20	< 20	< 20
5	20	S - gag	67	n.a. ⁴	n.a.
6	2	S - gag	63	n.a.	n.a.
7	0.	S - gag	57	n.a.	n.a.
8	0.02	S - gag	< 20	n.a.	n.a.
9	20	N ² - gag	43	n.a.	n.a.
10	2	N - gag	< 20	n.a.	n.a.
11	0.	N - gag	< 20	n.a.	n.a.
12	0.02	N - gag	< 20	n.a.	n.a.

1 = synthetic gag expression cassette (SEQ ID NO: 4)

2 = native gag expression cassette (SEQ ID NO: 1)

3 = geometric mean antibody titer

4 = not applicable

The results of the mouse immunizations with plasmid-DNAs show that the synthetic expression cassettes provide a clear improvement of immunogenicity relative to the native expression cassettes. Also, the second boost immunization induced a secondary immune response after two weeks (groups 1-3).

C. Cellular Immune Response

The frequency of specific cytotoxic T-lymphocytes (CTL) was evaluated by a standard chromium release assay of peptide pulsed Balb/c mouse CD4 cells. Gag expressing vaccinia virus infected CD-8 cells were used as a positive control (vvGag). Briefly, spleen cells (Effector cells, E) were obtained from the BALB/c mice immunized as described above (Table 8) were cultured, restimulated, and assayed for CTL activity against Gag

peptide-pulsed target cells as described (Doe, B., and Walker, C.M., *AIDS* 10(7):793-794, 1996). The HIV-1_{SF2} Gag peptide used was p7g SEQ ID NO:10. Cytotoxic activity was measured in a standard ⁵¹Cr release assay. Target (T) cells were cultured with effector (E) cells at various E:T ratios for 4 hours and the average cpm from duplicate wells was used to calculate percent specific ⁵¹Cr release. The results are presented in Table 9.

Cytotoxic T-cell (CTL) activity was measured in splenocytes recovered from the mice immunized with HIV Gag DNA (compare Effector column, Table 9, to immunization schedule, Table 8). Effector cells from the Gag DNA-immunized animals exhibited specific lysis of Gag p7g peptide-pulsed SV-BALB (MHC matched) targets cells indicative of a CTL response. Target cells that were peptide-pulsed and derived from an MHC-unmatched mouse strain (MC57) were not lysed (Table 9; MC/p7g).

Table 9

5

Table 9. Cytotoxic T-lymphocyte (CTL) responses in mice immunized with HIV-1 gag DNA

		Percent specific lysis of target cells*		
Immunization	E:T	SVBALB none	SVBALB p7g	RMA p7g
20 µg DNA gagmod	100:1	2	49	<1
	30:1	3	30	<1
	10:1	<1	14	<1
2 µg DNA gagmod	100:1	2	37	<1
	30:1	2	21	<1
	10:1	<1	13	<1
0.2 µg DNA gagmod	100:1	2	32	<1
	30:1	3	25	<1
	10:1	1	14	<1
0.02 µg DNA gagmod	100:1	1	17	<1
	30:1	1	16	<1
	10:1	1	8	<1
20 µg DNA gag native	100:1	2	49	<1
	30:1	2	24	<1
	10:1	1	12	<1
2 µg DNA gag native	100:1	<1	18	<1
	30:1	1	14	<1
	10:1	1	7	<1
0.2 µg DNA gag native	100:1	3	30	<1
	30:1	3	17	<1
	10:1	2	7	<1
0.02 µg DNA gag native	100:1	4	2	<1
	30:1	1	2	<1
	10:1	1	2	<1

*representative results of two animals per DNA-dose; positive CTL responses are indicated by boxed data

The results of the CTL assays show increased potency of synthetic Gag expression cassettes for induction of cytotoxic T-lymphocyte (CTL) responses by DNA immunization.

Example 9In vivo Immunization with Env polypeptidesA. Immunogenicity Study of US4 o-gp140 in Ras-3c Adjuvant System

5 Studies have been conducted using rabbits immunized with US4 o-gp140 purified as described above. Studies are also underway in animals to determine immunogenicity of US4 gp120, SF162 o-gp140 and SF162 gp120.

10 Two rabbits (#1 and #2) were immunized intramuscularly at 0, 4, 12 and 24 weeks with 50 μ g of US4 o-gp140 in the Ribi™ adjuvant system (RAS-3c), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL, Ribi Immunochem, Hamilton, MT).

15 In each experiment described herein, o-gp140 can be native, mutated and/or modified. Antibody responses directed against the US4 o-gp140 protein were measured by ELISA. Results are shown in Table 10.

Table 10

Rabbit/sample	Approximate o-gp140 ELISA titer
pre-immunization	0
#1: post1 (0 week immuniz)	400
#1: post2 (4 week immuniz)	15,000
#1: post3 (12 week immuniz)	50,000
#1: post4 (24 week immuniz)	100,000
#2: post1 (0 week immuniz)	600
#2: post2 (4 week immuniz)	12,000
#2: post3 (12 week immuniz)	25,000
#2: post4 (24 week immuniz)	55,000

The avidities of antibodies directed against the US4 o-gp140 protein were measured in a similar ELISA format employing successive washes with increasing concentrations of ammonium isothiocyanate. Results are shown in Table 11.

Table 11

Time of sample	Approx. Antibody avidity (NH ₄ HCN Conc. in M)
pre-immunization	0.02
post1 (0 week immuniz)	1.8
post2 (4 week immuniz)	3.5
post3 (12 week immuniz)	5.5
post4 (24 week immuniz)	5.1

These results show that US4 o-gp140 is highly immunogenic and able to induce substantial antibody responses after only one or two immunizations.

5 B. Immunogenicity of US4 o-gp140 in MF59-based Adjuvants

Groups of 4 rabbits were immunized intramuscularly at 0, 4, 12 and 24 weeks with various doses of US4 o-gp140 protein in three different MF59-based adjuvants (MF59 is described in International Publication No. WO 90/14837 and typically contains 5% Squalene, 0.5% Tween 80, and 0.5% Span 85). Antibody titers were measured post-third by ELISA using SF2 gp120 to coat the plates. QHC is a quill-based adjuvant (Iscotek, Uppsala, Sweden). Results are shown in Table 12.

Table 12

Antigen dose (μ g)	Adjuvant	Anti-gp120 _{SF2} Ab GMT*
12.5	MF59	7231
25	MF59	8896
50	MF59	12822
12.5	MF59/MPL	24146
25	MF59/MPL	27199
50	MF59/MPL	23059
50	MF59/MPL/QHC	31759

*GMT = geometric mean titer

Thus, adjuvanted o-gp140 generated antigen-specific antibodies. Further, the antibodies were shown to increased in avidity over time.

30 C. Neutralizing Antibodies

Neutralizing antibodies post-third immunization were measured against HIV-1 SF2 in a T-cell line adapted virus

(TCLA) assay and against PBMC-grown HIV-1 variants SF2, SF162 and 119 using the CCR5+ CEMx174 LTR-GFP reporter cell line, 5.25 (provided by N. Landau, Salk Institute, San Diego, CA) as target cells. Results are shown in Table 13.

5

Table 13

Neutralizing antibody responses in rabbits immunized with o-gp140.modUS4 protein

Group	Animal	SF2 TCLA*	SF2 PBMC#	SF162 PBMC#	119 PBMC#
Experiment 1					
o-gp140/ Ras-3c 50 mg	217	>640	100%	49	17
	218	>640	96	37	29
Experiment 2					
o-gp140/ MF59 50 mg	792	45	71	39	26
	793	50	87	26	4
	794	59	87	13	0
	795	128	92	15	0
o-gp140/ MF59 + MPL 50 mg	804	173	91	47	18
	805	134	93	28	4
	806	N.D.**	95	49	13
	807	441	100	31	15
o-gp140/MF59 + MPL + QHC 50 mg	808	465	98	46	40
	809	496	100	44	39
	810	>640	101	27	4
	811	92	92	24	37

*TCLA neutralizing antibody titers (50% inhibition).

**Not Determined

% Inhibition at 1:10 dilution of sera with any detectable non-specific inhibition in pre-bleeds subtracted.

35

The above studies in rabbits indicate that the US4 o-gp140 protein is highly immunogenic. When administered with adjuvant, this protein was able to induce substantial antibody responses after only one or two immunizations. Moreover, the adjuvanted o-gp140 protein was able to generate antigen-specific antibodies which increased in avidity after successive immunizations, and substantial neutralizing activity against T-cell line adapted HIV-1. Neutralizing activity was also observed against PBMC-grown primary HIV strains, including the difficult to neutralize CCR5 co-receptor (R5)-utilizing isolates, SF162 and 119.

Example 10

In Vivo Immunogenicity of Synthetic Env Expression

Cassettes

A. General Immunization Methods

To evaluate the immunogenicity of the synthetic Env expression cassettes, studies using guinea pigs, rabbits, mice, rhesus macaques and baboons were performed. The studies were structured as follows: DNA immunization alone (single or multiple); DNA immunization followed by protein immunization (boost); DNA immunization followed by Sindbis particle immunization; immunization by Sindbis particles alone.

B. Humoral Immune Response

The humoral immune response was checked in serum specimens from immunized animals with an anti-HIV Env antibody ELISAs (enzyme-linked immunosorbent assays) at various times post-immunization. The antibody titers of the sera were determined by anti-Env antibody ELISA as described above. Briefly, sera from immunized animals were

screened for antibodies directed against the HIV gp120 or gp140 Env protein. Wells of ELISA microtiter plates were coated

overnight with the selected Env protein and washed four times; subsequently, blocking was done with PBS-0.2% Tween (Sigma) for 2 hours. After removal of the blocking solution, 100 μ l of diluted mouse serum was added. Sera were tested at 1/25 dilutions and by serial 3-fold dilutions, thereafter. Microtiter plates were washed four times and incubated with a secondary, peroxidase-coupled anti-mouse IgG antibody (Pierce, Rockford, IL). ELISA plates were washed and 100 μ l of 3, 3', 5, 5'-tetramethyl benzidine (TMB; Pierce) was added per well. The optical density of each well was measured after 15 minutes. Titers are typically reported as the reciprocal of the dilution of serum that gave a half-maximum optical density (O.D.).

Example 11

DNA-immunization of Baboons Using Synthetic Gag

Expression Cassettes

A. Baboons

Four baboons were immunized 3 times (weeks 0, 4 and 8) bilaterally, intramuscular into the quadriceps using 1mg pCMVKM2.GagMod.SF2 plasmid-DNA (Example 1). The animals were bled two weeks after each immunization and a p24 antibody ELISA was performed with isolated plasma. The ELISA was performed essentially as described in Example 5 except the second antibody-conjugate was an anti-human IgG, g-chain specific, peroxidase conjugate (Sigma Chemical Co., St. Louis, MD 63178) used at a dilution of 1:500. Fifty μ g/ml yeast extract was added to the dilutions of plasma

samples and antibody conjugate to reduce non-specific background due to

preexisting yeast antibodies in the baboons. The antibody titer results are presented in Table 14.

5

Table 14

Immunization no.	Weeks	Antigen	wpi ^a / Baboon No.	Ab-titer ^b
10	0	gagmod DNA	0 w/219	< 10
			0 w/220	< 10
			0 w/221	< 10
			0 w/222	< 10
15	6		2 wp 1st/219	< 10
			2 wp 1st/220	< 10
			2 wp 1st/221	< 10
			2 wp 1st/222	15
20	14	gagmod DNA	2 wp 4th/219	< 10
			2 wp 4th/220	88
			2 wp 4th/221	< 10
			2 wp 4th/222	56
25	30	gagmod DNA	2 wp 5th/219	< 10
			2 wp 5th/220	391
			2 wp 5th/221	237
			2 wp 5th/222	222
30	46	gag VLP protein	2 wp 6th/219	753
			2 wp 6th/219	4330
			2 wp 6th/219	5000
			2 wp 6th/219	2881

^a wpi = weeks post immunization

^b geometric mean antibody titer

30

In Table 14, pre-bleed data are given as Immunization No. 0; data for bleeds taken 2 weeks post-first immunization are given as Immunization No. 1; data for bleeds taken 2 weeks post-second immunization are given as Immunization No. 2; and, data for bleeds taken 2 weeks post-third immunization are given as Immunization No. 3.

Further, lymphoproliferative responses to p24 antigen were also observed in baboons 221 and 222 two weeks post-fourth immunization (at week 14), and enhanced substantially post-boosting with VLP (at week 44 and 76).
5 Such proliferation results are indicative of induction of T-helper cell functions.

B. Rhesus Macaques

The improved potency of the codon-modified gag expression plasmid observed in mouse and baboon studies
10 was confirmed in rhesus macaques. Four of four macaques had detectable Gag-specific CTL after two or three 1 mg doses of modified gag plasmid. In contrast, in a previous study, only one of four macaques given 1 mg
15 doses of plasmid-DNA encoding the wild-type HIV-1_{SF2} Gag showed strong CTL activity that was not apparent until after the seventh immunization. Further evidence of the potency of the modified gag plasmid was the observation that CTL from two of the four rhesus macaques reacted
20 with three nonoverlapping Gag peptide pools, suggesting that as many as three different Gag peptides are recognized and indicating that the CTL response is polyclonal. Additional quantification and specificity studies are in progress to further characterize the T
25 cell responses to Gag in the plasmid-immunized rhesus macaques. DNA immunization of macaques with the modified gag plasmid did not result in significant antibody responses, with only two of four animals seroconverting at low titers. In contrast, in the same study the
30 majority of macaques in groups immunized with p55Gag protein seroconverted and had strong Gag-specific antibody titers. These data suggest that a prime-boost

strategy (DNA-prime and protein-boost) could be very promising for the induction of a strong CTL and antibody response.

5 In sum, these results demonstrate that the synthetic
Gag plasmid DNA is immunogenic in non-human primates.
When similar experiments were carried out using wild-type
Gag plasmid DNA no such induction of anti-p24 antibodies
was observed after four immunizations.

10

Example 12

DNA- and Protein Immunizations of Animals Using Env Expression Cassettes and Polypeptides

A. Guinea Pigs

Groups comprising six guinea pigs each were
15 immunized intramuscularly at 0, 4, and 12 weeks with
plasmid DNAs encoding the gp120.modUS4, gp140.modUS4,
gp140.modUS4.delV1, gp140.modUS4.delV2,
gp140.modUS4.delV1/V2, or gp160.modUS4 coding sequences
of the US4-derived Env. The animals were subsequently
20 boosted at 18 weeks with a single intramuscular dose of
US4 o-gp140.mut.modUS4 protein in MF59 adjuvant. Anti-
gp120 SF2 antibody titers (geometric mean titers) were
measured at two weeks following the third DNA
immunization and at two weeks after the protein boost.
25 Results are shown in Table 15.

Table 15

Group	GMT post-DNA immuniz.	GMT post-protein boost
gp120.modUS4	2098	9489
gp140.modUS4	190	5340
gp140.modUS4.delV1	341	7808
gp140.modUS4.delV2	386	8165
gp140.modUS4.delV1/V 2	664	8270
gp160.modUS4	235	9928

These results demonstrate the usefulness of the synthetic constructs to generate immune responses, as well as, the advantage of providing a protein boost to enhance the immune response following DNA immunization.

B. Rabbits

Rabbits were immunized intramuscularly and intradermally using a Bioject needleless syringe with plasmid DNAs encoding the following synthetic SF162 Env polypeptides: gp120.modSF162, gp120.modSF162.delV2, gp140.modSF162, gp140.modSF162.delV2, gp140.mut.modSF162, gp140.mut.modSF162.delV2, gp160.modSF162, and gp160.modSF162.delV2. Approximately 1 mg of plasmid DNA (pCMVlink) carrying the synthetic Env expression cassette was used to immunize the rabbits. Rabbits were immunized with plasmid DNA at 0, 4, and 12 weeks. At two weeks after the third immunization all of the constructs were shown to have generated significant antibody titers in the test animals. Further, rabbits immunized with constructs containing deletions of the V2 region

generally generated similar antibody titers relative to rabbits immunized with the companion construct still containing the V2 region.

The nucleic acid immunizations are followed by protein boosting with o-gp140.modSF162.delV2 (0.1 mg of purified protein) at 24 weeks after the initial immunization. Results are shown in Table 16.

Table 16

Group	GMT 2wks post-2nd DNA immunization	GMT 2wks post-3rd DNA immunization	GMT 2wks post-protein boost
gp120.modSF162	4573	5899	26033
gp120.modSF162.delV2	3811	3122	29606
gp140.modSF162	1478	710	12882
gp140.modSF162.delV2	1572	819	11067
gp140.mut.modSF162	1417	788	8827
gp140.mut.modSF162.delV2	1378	1207	13301
gp160.modSF162	23	81	7050
gp160.modSF162.delV2	85	459	11568

All constructs are highly immunogenic and generate substantial antigen binding antibody responses after only 2 immunizations in rabbits.

C. Baboons

Groups of four baboons were immunized intramuscularly with 1 mg doses of DNA encoding different forms of synthetic US4 gp140 (see the following table) at 0, 4, 8, 12, 28, and 44 weeks. The animals were also boosted twice with US4 0-gp140 protein (gp140.mut.modUS4) at 44 and 76 weeks using MF59 as adjuvant. Results are shown in Table 17.

Table 17				
Animal	Treatment	2 Wks Post 5th DNA immuniza- tion	2 Wks post 6th DNA (plus o- gp140 prot. immuniz.)	2 Wks post 7th DNA (o-gp140 protein only)
CY 215	gp140.modUS4	8.3	446	1813
CY 216		8.3	433	1236
CY 217		68	1660	2989
CY 218		101	2556	1610
Geomean:		26.2	951.4	1812.1
CY 219	gp140.modUS4 + p55gag.SF2	8.3	8.3	421
CY 220		8.3	8.3	3117
CY 221		8.3	954	871
CY 222		8.3	71	916
Geomean:		8.3	46.5	1011.5
CY 223	gp140.mut. modUS4	41.4	10497	46432
CY 224		8.3	979	470
CY 225		135	2935	3870
CY 226		47	1209	4009
Geomean:		68.3	2457.4	4289.6
CY 227	gp140TM. modUS4	8.3	56	5001
CY 228		8.3	806	1170
CY 229		8.3	48	3402
CY 230		8.3	38	6520
GMT*:		8.3	95.3	3375.3

*GMT = geometric mean titer

The results in Table 17 demonstrate the usefulness of the synthetic constructs to generate immune responses in primates such as baboons. In addition, all animals

showed evidence of antigen-specific (Env antigen) lymphoproliferative responses.

D. Rhesus Macaques

5 Two rhesus macaques (designated H445 and J408) were immunized with 1 mg of DNA encoding SF162 gp140 with a deleted V2 region (SF162.gp140.delV2) by intramuscular (IM) and intradermal (ID) routes at 0, 4, 8, and 28 weeks. Approximately 100 μ g of the protein encoded by
10 the SF162.gp140mut.delV2 construct was also administered in MF59 by IM delivery at 28 weeks.

ELISA titers are shown in Figure 61. Neutralizing antibody activity is shown Tables 18 and 19. Neutralizing antibody activity was determined against a
15 variety of primary HIV-1 isolates in a primary lymphocyte or "PBMC-based" assay (see the following tables). Further, the phenotypic co-receptor usage for each of the primary isolates is indicated. As can be seen in the tables neutralizing antibodies were detected against
20 every isolate tested, including the HIV-1 primary isolates (i.e., SF128A, 92US660, 92HT593, 92US657, 92US714, 91US056, and 91US054).

Table 18					
	Treatment		Bleed 0	Bleed 1	Bleed 2
Animal	1st Immunization	2nd Immunization	1st Imm'n	2nd Imm'n	2 Wks post 2nd
5	EO 456	(None)	8.3	45	309
	EO 457		8.3	254	460
	EO 458		8.3	8.3	93
	EO 459		8.3	43	45
	EO 460		8.3	8.3	274
10	EO 461	25µg 120mod DNA	8.3	47	1502
	EO 462		8.3	80	5776
	EO 463		8.3	89	3440
	EO 464		8.3	8.3	3347
	EO 465		8.3	69	1127
15	EO 466	(None)	8.3	63	102
	EO 467		8.3	112	662
	EO 468		8.3	94	459
	EO 469		8.3	58	48
	EO 470		8.3	95	355
20	EO 471	50µg 120mod DNA	8.3	110	9074
	EO 472		8.3	8.3	4897
	EO 473		8.3	49	4089
	EO 474		8.3	59	5280
	EO 475		8.3	8.3	929
25	EO 476	Sindbis/Env	8.3		653
	EO 477		8.3	87	22675
	EO 478		8.3	76	3869
	EO 479		8.3		1004
	EO 480		8.3	71	7080

Table 19					
	Treatment		Bleed 0	Bleed 1	Bleed 2
Animal	1st Immunization	2nd Immunization	1st Imm'n	2nd Imm'n	2 Wks post 2nd
EO 481	Sindbis/Env	(None)	8.3	8.3	8.3
EO 482			8.3	8.3	8.3
EO 483			8.3	78	103
EO 484			8.3	8.3	32
EO 485			8.3	76	207
EO 486	Sindbis/Env	Sindbis/Env	8.3	8.3	458
EO 487			8.3	8.3	345
EO 488			8.3	8.3	331
EO 489			8.3	103	111
EO 490			8.3	8.3	5636

Lymphoproliferative activity (LPA) was also determined by antigenic stimulation followed by uptake of ³H-thymidine in these animals and is shown in Table 20. Experiment 1 was performed at 14 weeks post third DNA immunization and Experiment 2 was performed at 2 weeks post fourth DNA immunization using DNA and protein. For gp120ThaiE, gp120SF2 and US4 o-gp140, appropriate background values were used to calculate Stimulation Indices (S.I.; Antigenic stimulation CPM/Background CPM).

Table 20

S.I.: Calculated as Ag CPM/Background CPM				
Animal/ exp#	gp120Thai E	gp120 SF2	env2-3SF2	o- gp140US4
J408/#1	2	1	1	5
H445/#1	1	1	1	6
J408/#2	1	1	2	3
H445/#2	0	0	3	2

As can be seen by the results presented in Table 20 lymphoproliferative responses to o-gp140.US4 antigen were also in all four animals at both experimental time points. Such proliferation results are indicative of induction of T-helper cell functions.

The results presented above demonstrate that the synthetic gp140.modSF162.delV2 DNA and protein are immunogenic in non-human primates.

Example 13

In vitro expression of recombinant Sindbis RNA and DNA containing the synthetic Gag or Env expression cassettes5 A. Synthetic Gag expression cassettes

To evaluate the expression efficiency of the synthetic Gag expression cassette in Alphavirus vectors, the synthetic Gag expression cassette was subcloned into both plasmid DNA-based and recombinant vector particle-based Sindbis virus vectors. Specifically, a cDNA vector construct for *in vitro* transcription of Sindbis virus RNA vector replicons (pRSIN-luc; Dubensky, et al., *J Virol.* 70:508-519, 1996) was modified to contain a *PmeI* site for plasmid linearization and a polylinker for insertion of
10
15
heterologous genes. A polylinker was generated using two oligonucleotides that contain the sites *XhoI*, *PmlI*, *ApaI*, *NarI*, *XbaI*, and *NotI* (XPANXNF, SEQ ID NO:17, and XPANXNR, SEQ ID NO:18).

The plasmid pRSIN-luc (Dubensky et al., *supra*) was
20
digested with *XhoI* and *NotI* to remove the luciferase gene insert, blunt-ended using Klenow and dNTPs, and purified from an agarose gel using GeneCleanII (Biol01, Vista, CA). The oligonucleotides were annealed to each other and ligated into the plasmid. The resulting construct
25
was digested with *NotI* and *SacI* to remove the minimal Sindbis 3'-end sequence and A₄₀ tract, and ligated with an approximately 0.4 kbp fragment from PKSSIN1-BV (WO 97/38087). This 0.4 kbp fragment was obtained by digestion of pKSSIN1-BV with *NotI* and *SacI*, and
30
purification after size fractionation from an agarose gel. The fragment contained the complete Sindbis virus 3'-end, an A₄₀ tract and a *PmeI* site for linearization. This new vector construct was designated SINBVE.

The synthetic HIV Gag coding sequence was obtained from the parental plasmid by digestion with *EcoRI*, blunt-ending with Klenow and dNTPs, purification with GeneCleanII, digestion with *Sall*, size fractionation on an agarose gel, and purification from the agarose gel using GeneCleanII. The synthetic Gag coding fragment was ligated into the SINBVE vector that had been digested with *XhoI* and *PmlI*. The resulting vector was purified using GeneCleanII and designated SINBVGag. Vector RNA replicons may be transcribed *in vitro* (Dubensky et al., *supra*) from SINBVGag and used directly for transfection of cells. Alternatively, the replicons may be packaged into recombinant vector particles by co-transfection with defective helper RNAs or using an alphavirus packaging cell line as described, for example, in U.S. Patent Numbers 5,843,723 and 5,789,245, and then administered *in vivo* as described..

The DNA-based Sindbis virus vector pDCMVSIN-beta-gal (Dubensky, et al., *J Virol.* 70:508-519, 1996) was digested with *Sall* and *XbaI*, to remove the beta-galactosidase gene insert, and purified using GeneCleanII after agarose gel size fractionation. The HIV Gag gene was inserted into the the pDCMVSIN-beta-gal by digestion of SINBVGag with *Sall* and *XhoI*, purification using GeneCleanII of the Gag-containing fragment after agarose gel size fractionation, and ligation. The resulting construct was designated pDSIN-Gag, and may be used directly for *in vivo* administration or formulated using any of the methods described herein.

BHK and 293 cells were transfected with recombinant Sindbis vector RNA and DNA, respectively. The supernatants and cell lysates were tested with the Coulter p24 capture ELISA (Example 2).

BHK cells were transfected by electroporation with recombinant Sindbis RNA. The expression of p24 (in ng/ml) is presented in Table 21. In the table, SINGag#1 and 2 represent duplicate measurements, and SIN β gal represents a negative control. Supernatants and lysates were collected 24h post transfection.

Table 21

Construct	Supernatant	Lysate
SIN β gal RNA	0	0
SINGag#1 RNA	7 ng	Max (approx. 1 μ g)
SINGag#2 RNA	1 ng	700 ng

293 cells were transfected using LT-1 (Example 2) with recombinant Sindbis DNA. Synthetic pCMVKM2GagMod.SF2 was used as a positive control. Supernatants and lysates were collected 48h post transfection. The expression of p24 (in ng/ml) is presented in Table 22.

Table 22

Construct	Supernatant	Lysate
SINGag DNA	3	30
pCMVKM2.GagMod.SF2 DNA	32	42

The results presented in Tables 21 and 22 demonstrate that Gag proteins can be efficiently expressed from both DNA and RNA-based Sindbis vector systems using the synthetic Gag expression cassette (p55Gag.mod).

B. Synthetic Env expression cassettes

To evaluate the expression efficiency of the synthetic Env expression cassette in Alphavirus vectors,

synthetic Env expression cassettes were subcloned into both plasmid DNA-based and recombinant vector particle-based Sindbis virus vectors as described above for Gag.

5 The synthetic HIV Env coding sequence was obtained from the parental plasmid by digestion with *SalI* and *XbaI*, size fractionation on an agarose gel, and purification from the agarose gel using GeneCleanII. The synthetic Env coding fragment was ligated into the SINBVE vector that had been digested with *XhoI* and *XbaI*. The
10 resulting vector was purified using GeneCleanII and designated SINBVEEnv. Vector RNA replicons may be transcribed *in vitro* (Dubensky et al., *supra*) from SINBVEEnv and used directly for transfection of cells. Alternatively, the replicons may be packaged into
15 recombinant vector particles by co-transfection with defective helper RNAs or using an alphavirus packaging cell line and administered as described above for Gag.

The DNA-based Sindbis virus vector pDCMVSIN-beta-gal (Dubensky, et al., *J Virol.* 70:508-519, 1996) was
20 digested with *SalI* and *XbaI*, to remove the beta-galactosidase gene insert, and purified using GeneCleanII after agarose gel size fractionation. The HIV Env gene was inserted into the the pDCMVSIN-beta-gal by digestion of SINBVEEnv with *XbaI* and *XhoI*, purification using
25 GeneCleanII of the Env-containing fragment after agarose gel size fractionation, and ligation. The resulting construct was designated pDSIN-Env, and may be used directly for *in vivo* administration or formulated using any of the methods described herein.

30 BHK and 293 cells were transfected with recombinant Sindbis vector RNA and DNA, respectively. The supernatants and cell lysates were tested by capture ELISA.

BHK cells were transfected by electroporation with recombinant Sindbis RNA. The expression of Env (in ng/ml) is presented in Table 23. In the table, the Sindbis RNA containing synthetic Env expression cassettes are indicated and β gal represents a negative control. Supernatants and lysates were collected 24h post transfection.

Table 23

Construct	Supernatant (Neat)ng/ml	Lysate (1:10 dilution)ng/ml
β gal RNA	0	0
gp140.modUS4	726	7147
gp140.modSF162	3529	7772
gp140.modUS4.delV1/V2	1738	6526
gp140.modUS4.delV2	960	3023
gp140.modSF162.delV2	2772	3359

293 cells were transfected using LT-1 mediated transfection (PanVera) with recombinant Sindbis DNA containing synthetic expression cassettes of the present invention and β gal sequences as a negative control. Supernatants and lysates were collected 48h post transfection. The expression of Env (in ng/ml) is presented in Table 24.

Table 24

Construct	Supernatant (Neat)ng/ml	Lysate (1:10 dilution)ng/ml
β gal	0	0
gp140.modSF162.delV2	1977	801
gp140.modSF162	949	746

The results presented in Tables 23 and 24 demonstrated that Env proteins can be efficiently expressed from both DNA and RNA-based Sindbis vector systems using the synthetic Env expression cassettes of the present invention.

Example 14

A. In vivo Immunization with Gag-containing DNA and/or Sindbis particles

CB6F1 mice were immunized intramuscularly at 0 and 4 weeks with plasmid DNA and/or Sindbis vector RNA-containing particles each containing GagMod.SF2 sequences as indicated in Table 25. Animals were challenged with recombinant vaccinia expressing SF2 Gag at 3 weeks post second immunization (at week 7). Spleens were removed from the immunized and challenged animals 5 days later for a standard ^{51}C release assay for CTL activity. Values shown in Table 25 indicate the results from the spleens of three mice from each group. The boxed values in Table 25 indicate that all groups of mice receiving immunizations with pCMVKm2.GagMod.SF2 DNA and/or SindbisGagMod.SF2 virus particles either alone or in combinations showed antigen-specific CTL activity.

Table 25

Cytotoxic T-lymphocyte (CTL) responses in mice immunized with HIV-1 gagmod DNA and Sindbis gagmod virus particles

5	Immunization	E:T	Percent specific lysis of target cells*		
			SVBALB none	SVBALB p7g	RMA p7g
10	pCMVKm2.GagMod.SF2 DNA ^a	100:1	5	20	1
	at 0, 4 wks	25:1	5	20	<1
		6:1	4	8	<1
15	SindbisGagMod.SF2 virus particles ^b	100:1	10	49	<1
	at 0, 4 weeks	25:1	7	20	<1
		6:1	5	12	<1
20	pCMVKm2.GagMod.SF2 DNA at 0 wks	100:1	9	58	<1
	SindbisGagMod.SF2 virus particles at 4 wks	25:1	7	42	2
		6:1	4	13	<1
25	SindbisGagMod.SF2 virus particles at 4 wks	100:1	5	38	<1
		25:1	4	18	<1
	pCMVKm2.GagMod.SF2 DNA at 0 wks	6:1	3	13	1

^a 20 µg

^b 10⁷ particles

* Challenge with recombinant vaccinia virus expressing HIV-1SF2 Gag at 3 weeks post second immunization (week 7). Spleens taken 5 days later. Ex vivo CTL assay performed by standard ⁵¹Cr release assay. Values seen represent results from 3 pooled mouse spleens per group

B. In vivo Immunization with Env-containing DNA and/or Sindbis particles

Balb/C mice were immunized intramuscularly at 0 and 4 weeks (as shown in the following table) with plasmid DNA and/or Sindbis-virus RNA-containing particles each containing gp120.modUS4 sequences. Treatment regimes and antibody titers are shown in Table 26. Antibody titers were determined by ELISA using gp120 SF2 protein to coat the plates.

Table 26					
	Treatment		Bleed 0	Bleed 1 (8 wks)	Bleed 2 (10 wks)
Animal	1st Immunization	2nd Immunization	1st Imm'n	2nd Imm'n	2 Wks post 2nd
EO 456	25 μ g 120mod DNA	(None)	8.3	45	309
EO 457			8.3	254	460
EO 458			8.3	8.3	93
EO 459			8.3	43	45
EO 460			8.3	8.3	274
EO 461	25 μ g 120mod DNA	25 μ g 120mod DNA	8.3	47	1502
EO 462			8.3	80	5776
EO 463			8.3	89	3440
EO 464			8.3	8.3	3347
EO 465			8.3	69	1127
EO 466	50 μ g 120mod DNA	(None)	8.3	63	102
EO 467			8.3	112	662
EO 468			8.3	94	459
EO 469			8.3	58	48
EO 470			8.3	95	355
EO 471	50 μ g 120mod DNA	50 μ g 120mod DNA	8.3	110	9074
EO 472			8.3	8.3	4897
EO 473			8.3	49	4089
EO 474			8.3	59	5280
EO 475			8.3	8.3	929
EO 476	25 μ g 120mod DNA	Sindbis/Env	8.3		653
EO 477			8.3	87	22675
EO 478			8.3	76	3869
EO 479			8.3		1004
EO 480			8.3	71	7080
EO 481	Sindbis/Env	(None)	8.3	8.3	8.3
EO 482			8.3	8.3	8.3
EO 483			8.3	78	103
EO 484			8.3	8.3	32
EO 485			8.3	76	207
EO 486	Sindbis/Env	Sindbis/Env	8.3	8.3	458
EO 487			8.3	8.3	345
EO 488			8.3	8.3	331
EO 489			8.3	103	111
EO 490			8.3	8.3	5636

As can be seen from the data presented above, all of the mice generally demonstrated substantial immunological responses by bleed number 2. For Env, the best results were obtained using either (i) 50 μ g of gp120.modUS4 DNA for the first immunization followed by a second

immunization using 50 μ g of gp120.modUS4 DNA, or (ii) 25 μ g of gp120.modUS4 DNA for the first immunization followed by a second immunization using 10^7 pfus of Sindbis.

- 5 The results presented above demonstrate that the Env and Gag proteins of the present invention are effective to induce an immune response using Sindbis vector systems which include the synthetic Env (e.g., gp120.modUS4) or Gag expression cassettes.

10

Example 15

Co-Transfection of Env and Gag as Monocistronic and Bicistronic Constructs

- DNA constructs encoding (i) wild-type US4 and SF162 Env polypeptides, (ii) synthetic US4 and SF162 Env polypeptides (gp160.modUS4, gp160.modUS4.delV1/V2, gp160.modSF162, and gp120.modSF162.delV2), and (iii) SF2gag polypeptide (i.e., the Gag coding sequences obtained from the SF2 variant or optimized sequences corresponding to the gagSF2 -- gag.modSF2) were prepared. These monocistronic constructs were co-transfected into 293T cells in a transient transfection protocol using the following combinations: gp160.modUS4; gp160.modUS4 and gag.modSF2; gp160.modUS4.delV1/V2; gp160.modUS4.delV1/V2 and gag.modSF2; gp160.modSF162 and gag.modSF2; gp120.modSF162.delV2 and gag.modSF2; and gag.modSF2 alone.

- Further several bicistronic constructs were made where the coding sequences for Env and Gag were under the control of a single CMV promoter and, between the two coding sequences, an IRES (internal ribosome entry site (EMCV IRES); Kozak, M., Critical Reviews in Biochemistry and Molecular Biology 27(45):385-402, 1992; Witherell, G.W., et al., Virology 214:660-663, 1995) sequence was

introduced after the Env coding sequence and before the Gag coding sequence. Those constructs were as follows:
gp160.modUS4.gag.modSF2, SEQ ID NO:73 (Figure 61);
gp160.modUSF162.gag.modSF2, SEQ ID NO:74 (Figure 62);
5 gp160.modUS4.delV1/V2.gag.modSF2, SEQ ID NO:75 (Figure 63); and gp160.modSF162.delV2.gag.modSF2, SEQ ID NO:76 (Figure 64).

Supernatants from cell culture were filtered through 0.45 μ m filters then ultracentrifuged for 2 hours at
10 24,000 rpm (140,000Xg) in an SW28 rotor through a 20% sucrose cushion. The pelleted materials were suspended and layered on a 20-60% sucrose gradient and spun for 2 hours at 40,000 rpm (285,000Xg) in an SW41Ti rotor. Gradients were fractionated into 1.0 ml samples. A total
15 of 9-10 fractions were typically collected from each DNA transfection group.

The fractions were tested for the presence of the Env and Gag proteins (across all fractions). These results demonstrated that the appropriate proteins were
20 expressed in the transfected cells (i.e., if an Env coding sequence was present the corresponding Env protein was detected; if a Gag coding sequence was present the corresponding Gag protein was detected).

Virus like particles (VLPs) were known to be present
25 through a selected range of sucrose densities. Chimeric virus like particles (VLPs) were formed using all the tested combinations of constructs containing both Env and Gag. Significantly more protein was found in the supernatant collected from the cells transfected with
30 "gp160.modUS4.delV1/V2 and gag.modSF2" than in all the other supernatants.

Western blot analysis was also performed on sucrose gradient fractions from each transfection. The results show that bicistronic plasmids gave lower amounts of VLPs

than the amounts obtained using co-transfection with monocistronic plasmids.

In order to verify the production of chimeric VLPs by these cell lines the following electron microscopic
5 analysis was carried out.

293T cells were plated at a density of 60-70% confluence in 100 mm dishes on the day before transfection. The cells were transfected with 10 μ g of DNA in transfection reagent LT1 (Panvera Corporation, 545
10 Science Dr., Madison, WI). The cells were incubated overnight in reduced serum medium (opti-MEM, Gibco-BRL, Gaithersburg, MD). The medium was replaced with 10% fetal calf serum, 2% glutamine in IMDM in the morning of the next day and the cells were incubated for 65 hours.
15 Supernatants and lysates were collected for analysis as described above (see Example 2).

The fixed, transfected 293T cells and purified ENV-GAG VLPs were analyzed by electron microscopy. The cells were fixed as follows. Cell monolayers were washed twice
20 with PBS and fixed with 2% glutaraldehyde. For purified VLPs, gradient peak fractions were collected and concentrated by ultracentrifugation (24,000 rpm) for 2 hours. Electron microscopic analysis was performed by Prof. T.S. Benedict Yen (Veterans Affairs, Medical
25 Center, San Francisco, CA).

Electron microscopy was carried out using a transmission electron microscope (Zeiss 10c). The cells were pre-stained with osmium and stained with uranium acetate and lead citrate. Immunostaining was performed
30 to visualize envelope on the VLP. The magnification was 100,000X.

Figures 65A-65F show micrographs of 293T cells transfected with the following constructs: Figure 65A, gag.modSF2; Figure 65B, gp160.modUS4; Figure 65C,

gp160.modUS4.delV1/V2.gag.modSF2 (bicistronic Env and
Gag); Figures 65D and 65E, gp160.modUS4.delV1/V2 and
gag.modSF2; and Figure 65F, gp120.modSF162.delV2 and
gag.modSF2. In the figures, free and budding immature
5 virus-like-particles (VLPs) of the expected size
(approximately 100 nm) decorated with the Env protein
were seen. In sum, gp160 polypeptides incorporate into
Gag VLPs when constructs were co-transfected into cells.
The efficiency of incorporation is 2-3 fold higher when
10 constructs encoding V-deleted Env polypeptides from high
synthetic expression cassettes are used.

Although preferred embodiments of the subject
invention have been described in some detail, it is
understood that obvious variations can be made without
15 departing from the spirit and the scope of the invention
as defined by the appended claims.

What Is Claimed Is:

1. An expression cassette, comprising
5 a polynucleotide sequence encoding a polypeptide including an HIV Gag polypeptide, wherein the polynucleotide sequence encoding said Gag polypeptide comprises a sequence having at least 90% sequence identity to the sequence presented as SEQ ID NO:20.
10
2. The expression cassette of claim 1, comprising, a polynucleotide sequence encoding a polypeptide including an HIV Gag polypeptide, wherein the polynucleotide sequence encoding said Gag polypeptide
15 comprises a sequence having at least 90% sequence identity to the sequence presented as SEQ ID NO:9.
3. The expression cassette of claim 1, wherein said polynucleotide sequence encoding a polypeptide including
20 an HIV Gag polypeptide comprises a sequence having at least 90% sequence identity to the sequence presented as SEQ ID NO:4.
4. The expression cassette of claim 1, wherein said
25 polynucleotide sequence further includes a polynucleotide sequence encoding an HIV protease polypeptide.
5. The expression cassette of claim 4, wherein the
30 nucleotide sequence encoding said polypeptide comprises a sequence having at least 90% sequence identity to a sequence selected from the group consisting of: SEQ ID NO:5, SEQ ID NO:78, and SEQ ID NO:79.
6. The expression cassette of claim 1, wherein said

polynucleotide sequence further includes a polynucleotide sequence encoding an HIV *reverse transcriptase* polypeptide.

5 7. The expression cassette of claim 6, wherein the nucleotide sequence encoding said polypeptide comprises a sequence having at least 90% sequence identity to a sequence selected from the group consisting of: SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, and SEQ
10 ID NO:84.

 8. The expression cassette of claim 1, wherein said polynucleotide sequence further includes a polynucleotide sequence encoding an HIV *tat* polypeptide.
15

 9. The expression cassette of claim 8, wherein the nucleotide sequence encoding said polypeptide comprises a sequence having at least 90% sequence identity to a sequence selected from the group consisting of: SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88 and SEQ ID NO:89.
20

 10. The expression cassette of claim 1, wherein said polynucleotide sequence further includes a polynucleotide sequence encoding an HIV *polymerase* polypeptide, wherein the nucleotide sequence encoding said polypeptide comprises a sequence having at least 90% sequence identity to the sequence presented as SEQ ID NO:6.
25

 11. The expression cassette of claim 1, wherein said polynucleotide sequence further includes a polynucleotide sequence encoding an HIV *polymerase* polypeptide, wherein (i) the nucleotide sequence encoding said polypeptide comprises a sequence having at least 90%
30

sequence identity to the sequence presented as SEQ ID NO:4, and (ii) wherein the sequence is modified by deletions of coding regions corresponding to reverse transcriptase and integrase.

5

12. The expression cassette of claim 11, wherein said polynucleotide sequence preserves T-helper cell and CTL epitopes.

10

13. The expression cassette of claim 1, wherein said polynucleotide sequence further includes a polynucleotide sequence encoding an HCV core polypeptide, wherein the nucleotide sequence encoding said polypeptide comprises a sequence having at least 90% sequence

15

identity to the sequence presented as SEQ ID NO:7.

20

14. An expression cassette, comprising a polynucleotide sequence encoding a polypeptide including an HIV *Env* polypeptide, wherein the polynucleotide sequence encoding said *Env* polypeptide comprises a sequence having at least 90% sequence identity to SEQ ID NO:71 (Figure 58) or SEQ ID NO:72 (Figure 59).

25

15. The expression cassette of claim 14, wherein said *Env* polypeptide includes sequences flanking a V1 region but has a deletion in the V1 region itself.

30

16. The expression cassette of claim 15, wherein the polynucleotide sequence encoding the polypeptide comprises the sequence presented as SEQ ID NO:65 (Figure 52 gp160.modUS4.delV1).

17. The expression cassette of claim 14, wherein

said Env polypeptide includes sequences flanking a V2 region but has a deletion in the V2 region itself.

18. The expression cassette of claim 17, wherein
5 the polynucleotide sequence encoding the polypeptide is selected from the group consisting of: SEQ ID NO:60 (Figure 47); and SEQ ID NO:66 (Figure 53).

19. The expression cassette of claim 17, wherein
10 the polynucleotide sequence encoding the polypeptide is selected from the group consisting of: SEQ ID NO:34 (Figure 20); SEQ ID NO:37 (Figure 24); SEQ ID NO:40 (Figure 27); SEQ ID NO:43 (Figure 30); SEQ ID NO:46 (Figure 33); SEQ ID NO:49 (Figure 36); and SEQ ID NO:76
15 (Figure 64).

20. The expression cassette of claim 14, wherein
said Env polypeptide includes sequences flanking a V1/V2 region but has a deletion in the V1/V2 region itself.

20

21. The expression cassette of claim 20, wherein
the polynucleotide sequence encoding the polypeptide is selected from the group consisting of: SEQ ID NO:59 (Figure 46); SEQ ID NO:61 (Figure 48); SEQ ID NO:67
25 (Figure 54); and SEQ ID NO:75 (Figure 63).

22. The expression cassette of claim 20, wherein
the polynucleotide sequence encoding the polypeptide is selected from the group consisting of: SEQ ID NO:35
30 (Figure 21); SEQ ID NO:38 (Figure 25); SEQ ID NO:41 (Figure 28); SEQ ID NO:44 (Figure 31); SEQ ID NO:47 (Figure 34) and SEQ ID NO:50 (Figure 37).

23. The expression cassette of claim 14, wherein said *Env* polypeptide has a mutated cleavage site that prevents the cleavage of a gp140 polypeptide into a gp120 polypeptide and a gp41 polypeptide.

5

24. The expression cassette of claim 23, wherein the polynucleotide sequence encoding the polypeptide is selected from the group consisting of: SEQ ID NO:57 (Figure 44); SEQ ID NO:61 (Figure 48); and SEQ ID NO:63 (Figure 50).

10

25. The expression cassette of claim 23, wherein the polynucleotide sequence encoding the polypeptide is selected from the group consisting of: SEQ ID NO:39 (Figure 26); SEQ ID NO:40 (Figure 27); SEQ ID NO:41 (Figure 28); SEQ ID NO:42 (Figure 29); SEQ ID NO:43 (Figure 30); SEQ ID NO:44 (Figure 31); SEQ ID NO:45 (Figure 32); SEQ ID NO:46 (Figure 33); and SEQ ID NO:47 (Figure 34).

15
20

26. The expression cassette of claim 14, wherein said *Env* polypeptide includes a gp160 *Env* polypeptide or a polypeptide derived from a gp160 *Env* polypeptide.

25

27. The expression cassette of claim 26, wherein the polynucleotide sequence encoding the polypeptide is selected from the group consisting of: SEQ ID NO:64 (Figure 51); SEQ ID NO:65 (Figure 52); SEQ ID NO:66 (Figure 53); SEQ ID NO:67 (Figure 54); SEQ ID NO:68 (Figure 55); SEQ ID NO:75 (Figure 63); and SEQ ID NO:73 (Figure 61).

30

28. The expression cassette of claim 26, wherein

the polynucleotide sequence encoding the polypeptide is selected from the group consisting of: SEQ ID NO:48 (Figure 35); SEQ ID NO:49 (Figure 36); SEQ ID NO:50 (Figure 37); SEQ ID NO:76 (Figure 64); and SEQ ID NO:74 (Figure 62).

29. The expression cassette of claim 14, wherein said *Env* polypeptide includes a gp140 *Env* polypeptide or a polypeptide derived from a gp140 *Env* polypeptide.

10

30. The expression cassette of claim 29, wherein the polynucleotide sequence encoding the polypeptide is selected from the group consisting of: SEQ ID NO:56 (Figure 43); SEQ ID NO:57 (Figure 44); SEQ ID NO:58 (Figure 45); SEQ ID NO:59 (Figure 46); SEQ ID NO:60 (Figure 47); SEQ ID NO:61 (Figure 48); SEQ ID NO:62 (Figure 49); and SEQ ID NO:63 (Figure 50).

31. The expression cassette of claim 29, wherein the polynucleotide sequence encoding the polypeptide is selected from the group consisting of: SEQ ID NO:36 (Figure 23); SEQ ID NO:37 (Figure 24); SEQ ID NO:38 (Figure 25); SEQ ID NO:39 (Figure 26); SEQ ID NO:40 (Figure 27); SEQ ID NO:41 (Figure 28); SEQ ID NO:42 (Figure 29); SEQ ID NO:43 (Figure 30); SEQ ID NO:44 (Figure 31); SEQ ID NO:45 (Figure 32); SEQ ID NO:46 (Figure 33); and SEQ ID NO:47 (Figure 34).

32. The expression cassette of claim 14, wherein said *Env* polypeptide includes a gp120 *Env* polypeptide or a polypeptide derived from a gp120 *Env* polypeptide.

33. The expression cassette of claim 32, wherein the polynucleotide sequence encoding the polypeptide is selected from the group consisting of: SEQ ID NO:54 (Figure 41); and SEQ ID NO:55 (Figure 42).

5

34. The expression cassette of claim 32, wherein the polynucleotide sequence encoding the polypeptide is selected from the group consisting of: SEQ ID NO:33 (Figure 19); SEQ ID NO:34 (Figure 20); and SEQ ID NO:35 (Figure 21).

10

35. The expression cassette of claim 14, wherein the polynucleotide sequence encoding the polypeptide is selected from the group consisting of: SEQ ID NO:55 (Figure 42); SEQ ID NO:62 (Figure 49); SEQ ID NO:63 (Figure 50); and SEQ ID NO:68 (Figure 55).

15

36. A recombinant expression system for use in a selected host cell, comprising, an expression cassette of any of claims 1-35, and wherein said polynucleotide sequence is operably linked to control elements compatible with expression in the selected host cell.

20

37. The recombinant expression system of claim 36, wherein said control elements are selected from the group consisting of a transcription promoter, a transcription enhancer element, a transcription termination signal, polyadenylation sequences, sequences for optimization of initiation of translation, and translation termination sequences.

25

30

38. The recombinant expression system of claim 36, wherein said transcription promoter is selected from the

group consisting of CMV, CMV+intron A, SV40, RSV, HIV-Ltr, MMLV-ltr, and metallothionein.

39. A cell comprising an expression cassette of any
5 of claims 1-35, and wherein said polynucleotide sequence is operably linked to control elements compatible with expression in the selected cell.

40. The cell of claim 39, wherein the cell is a
10 mammalian cell.

41. The cell of claim 40, wherein the cell is selected from the group consisting of BHK, VERO, HT1080, 293, RD, COS-7, and CHO cells.

42. The cell of claim 41, wherein said cell is a
15 CHO cell.

43. The cell of claim 39, wherein the cell is an
20 insect cell.

44. The cell of claim 43, wherein the cell is either *Trichoplusia ni* (Tn5) or Sf9 insect cells.

45. The cell of claim 39, wherein the cell is a
25 bacterial cell.

46. The cell of claim 39, wherein the cell is a
30 yeast cell.

47. The cell of claim 39, wherein the cell is a plant cell.

48. The cell of claim 39, wherein the cell is an antigen presenting cell.

49. The cell of claim 48, wherein the lymphoid cell
5 is selected from the group consisting of macrophage, monocytes, dendritic cells, B-cells, T-cells, stem cells, and progenitor cells thereof.

50. The cell of claim 39, wherein the cell is a
10 primary cell.

51. The cell of claim 39, wherein the cell is an immortalized cell.

52. The cell of claim 39, wherein the cell is a
15 tumor-derived cell.

53. A method for producing a polypeptide including HIV Gag polypeptide sequences, said method comprising,
20 incubating the cells of claim 39, under conditions for producing said polypeptide.

54. A method for producing virus-like particles (VLPs), comprising,
25 incubating the cells of claim 39, under conditions for producing said VLPs.

55. A method for producing a composition of virus-like particles (VLPs), comprising,
30 (a) incubating the cells of claim 39, under conditions for producing said VLPs; and
(b) substantially purifying said VLPs to produce a composition of VLPs.

56. A cell line useful for packaging lentivirus vectors, comprising

5 suitable host cells that have been transfected with
an expression vector containing an expression cassette of
any of claims 1-35, and wherein said polynucleotide
sequence is operably linked to control elements
compatible with expression in the host cell.

10 57. The cell line of claim 56, wherein suitable
host cells have been transfected with an expression
vector containing the expression cassette of any of
claims 1-13.

15 58. The cell line of claim 56, wherein suitable
host cells have been transfected with an expression
vector containing the expression cassette of claim 1-3.

20 59. The cell line of claim 56, wherein suitable
host cells have been transfected with an expression
vector containing the expression cassette of claim 14-35.

60. A gene delivery vector for use in a Mammalian subject, comprising

25 a suitable gene delivery vector for use in said
subject, wherein the vector comprises an expression
cassette of any of claims 1-35, and wherein said
polynucleotide sequence is operably linked to control
elements compatible with expression in the subject.

30 61. A method of DNA immunization of a subject,
comprising,

introducing a gene delivery vector of claim 60 into
said subject under conditions that are compatible with
expression of said expression cassette in said subject.

62. The method of claim 61, wherein said gene delivery vector is a nonviral vector.

5 63. The method of claim 61, wherein said vector is delivered using a particulate carrier.

64. The method of claim 63, wherein said vector is coated on a gold or tungsten particle and said coated
10 particle is delivered to said subject using a gene gun.

65. The method of claim 63, wherein said vector is encapsulated in a liposome preparation.

15 66. The method of claim 61, wherein said vector is a viral vector.

67. The method of claim 66, wherein said viral vector is a retroviral vector.
20

68. The method of claim 67, wherein said viral vector is a lentiviral vector.

69. The method of claim 61, wherein said subject is
25 a mammal.

70. The method of claim 69, wherein said mammal is a human.

30 71. A method of generating an immune response in a subject, comprising
transfecting cells of said subject a gene delivery vector of claim 60, under conditions that permit the expression of said polynucleotide and production of said

polypeptide, thereby eliciting an immunological response to said polypeptide.

72. The method of claim 71, wherein said vector is
5 a nonviral vector.

73. The method of claim 72, wherein said vector is delivered using a particulate carrier.

10 74. The method of claim 73, wherein said vector is coated on a gold or tungsten particle and said coated particle is delivered to said vertebrate cell using a gene gun.

15 75. The method of claim 73, wherein said vector is encapsulated in a liposome preparation.

20 76. The method of claim 71, wherein said vector is a viral vector.

77. The method of claim 76, wherein said viral vector is a retroviral vector.

25 78. The method of claim 77, wherein said viral vector is a lentiviral vector.

79. The method of claim 71, wherein said subject is a mammal.

30 80. The method of claim 79, wherein said mammal is a human.

81. The method of claim 71, wherein said transfecting is done ex vivo and said transfected cells

are reintroduced into said subject.

82. The method of claim 71, wherein said transfecting is done *in vivo* in said subject.

5

83. The method of claim 71, where said immune response is a humoral immune response.

84. The method of claim 71, where said immune response is a cellular immune response.

10

85. A gene delivery vector comprising an alphavirus vector construct, wherein said alphavirus construct comprises an expression cassette according to any one of claims 1 through 35.

15

86. The gene delivery vector of claim 85, wherein the alphavirus vector construct is a cDNA vector construct.

20

87. The gene delivery vector of claim 85, wherein the alphavirus comprises a recombinant alphavirus particle preparation.

88. The gene delivery vector of claim 85, wherein the vector comprises a eukaryotic layered vector initiation system.

25

89. A method of stimulating an immune response in a subject comprising administering the gene delivery vector of any one of claims 85 through 88 in an amount effective to stimulate an immune response in said subject.

30

90. The method of claim 89, wherein the gene

delivery vector is administered intramuscularly, intramucosally, intranasally, subcutaneously, intradermally, transdermally, intravaginally, intrarectally, orally or intravenously.

5

1 / 131

orig.gagSF2

ATGGGTGCGAGAGCGTCGGTATTAAGCGGGGGAGAATTAGATAAATGGGAAAAAATTCGGTTAAGGCCAGGGGGAAAG

AAAAAATATAAGTTAAACATATAGTATGGGCAAGCAGGGAGCTAGAACGATTTCGCAGTCAATCCTGGCCTGTTAGAA
Inact. 1
G G C C G C C

ACATCAGAAGGCTGCAGACAAATATTGGGACAGCTACAGCCATCCCTTCAGACAGGATCAGAGAACTTAGATCATTAG
Inact. 2
G G C C

TATAATACAGTAGCAACCCCTCTATTGTGTACATCAAAGGATAGATGTAAAGGACACCAAGGAAGCTTTAGAGAAGATA
Inact. 3
C GC C C G

GAGGAAGAGCAAAACAAAGTAAGAAAAAGGCACAGCAAGCAGCAGCTGCAGCTGGCACAGGAAACAGCAGCCAGGTC
Inact. 4
GTCC G C G

AGCCAAAATTACCCTATAGTGCAGAACCTACAGGGGCAAATGGTACATCAGGCCATATCACCTAGAACTTTAAATGCA

TGGGTAAAAGTAGTAGAAGAAAAGGCTTTCAGCCCAGAAGTAATACCCATGTTTTTCAGCATTATCAGAAGGAGCCACC

CCACAGATTTAAACACCATGCTAAACACAGTGGGGGGACATCAAGCAGCCATGCAAATGTTAAAGAGACTATCAAT
Inact. 5
G CC G G T G C

GAGGAAGCTGCAGAAATGGGATAGAGTGCATCCAGTGCATGCAGGGCCTATTGCACCAGGCCAAATGAGAGAACCAAGG

GGAAGTGACATAGCAGGAACCTACTAGTACCCTTCAGGAACAAATAGGATGGATGACAAATAATCCACCTATCCCAGTA

GGAGAAATCTATAAAGATGGATAATCCTGGGATTAAATAAAATAGTAAGATGTATAGCCCTACCAGCATTCTGGAC
Inact. 6
G C G G Inact. 7
G C G C G G

ATAAGACAAGGACCAAAGGAACCCCTTTAGAGATTATGTAGACCGTTCTATAAACTCTAAGAGCGAACAAGCTTCA
Inact. 8
C CC G G T

CAGGATGTAAAAAATTGGATGACAGAAACCTTGTGGTCCAAATGCAAACCCAGATTGTAAGACTATTTTAAAGCA

TTGGGACCCAGCAGCTACACTAGAAGAAATGATGACAGCATGTCAGGGAGTGGGGGGACCCGGCCATAAAGCAAGAGTT
C C C

TTGGCTGAAGCCATGAGCCAAGTAACAAATCCAGCTAACATAATGATGCAGAGAGGCAATTTTAGGAACCAAAGAAAG

ACTGTTAAGTGTTTCAATTGTGGCAAAGAAGGGCACATAGCCAAAAATTGCAGGGCCCCTAGGAAAAAGGGCTGTTGG

AGATGTGGAAGGGAAGGACACCAAATGAAAGATTGCACTGAGAGACAGGCTAATTTTTTAGGGAAGATCTGGCCTTCC

TACAAGGGAAGGCCAGGGAATTTTCTTCAGAGCAGACCAGAGCCAACAGCCCCACCAGAAGAGAGCTTCAGGTTTGGG

GAGGAGAAAAACAACTCCCTCTCAGAAGCAGGAGCCGATAGACAAGGAAGTGTATCCTTTAACTTCCCTCAGATCACTC

TTTGGCAACGACCCCTCGTCACAATAA

FIG. 1

SUBSTITUTE SHEET (RULE 26)

native HIV-1SF2 gag-protease

2 / 131

From here codon optimization + inactivation (GP1) and (GP2)

ATGGGTGCGAGAGCGTCGGTATTAAGCGGGGAGAATTAGATAAATGGGAAAAAATTCGGTTAAGGCCAGGGGGAAAG

Inact.1
AATAATATAAGTTAAACATATGTATGGGCAAGCAGGGAGCTAGAACGATTTCGCAGTCAATCCTGGCCTGTTAGAA
G G C C G C G

Inact.2
ACATCAGAAGGCTGCAGACAAATATTGGGACAGCTACAGCCATCCCTTCAGACAGGATCAGAACTTAGATCATTAGAA
G G C C

Inact.2
TATAATACAGTAGCAACCCTCTATTGTGTACATCAAAGGATAGATGTAAAGACACCAAGGAAGCTTTAGAGAAGATA
C

Inact.3
TCAAAGGATAGATGTAAAGACACCAAGGAAGCTTTAGAGAAGATA
C GC C C G

Inact.4
AAGTAAGAAAAAGGCACAGCAAGCAGCAGCTGCAGCTGGCACAGGAAACAGCAGCCAGGTC
GTCC G C G

GAGGAAGAGCAAAACAAAGTAAGAAAAAGGCACAGCAAGCAGCAGCTGCAGCTGGCACAGGAAACAGCAGCCAGGTC

AGCCAAAATTACCTTATAGTGCAGAACCTACAGGGGCAAATGGTACATCAGGCCATATCACCTAGAACTTTAAATGCA

TGGGTAAAAGTAGTAGAAGAAAAGGCTTTCAGCCCAGAAGTAATACCCATGTTTTTCAGCATTATCAGAAGGAGCCACC

Inact.5
CCACAGATTTAAACACCATGCTAAACACAGTGGGGGGACATCAAGCAGCCATGCAAATGTTAAAAGAGACTATCAAT
G CC G G T G G

GAGGAAGCTGCAGAATGGGATAGAGTGCATCCAGTGCATGCAGGGCCTATTGCACCAGGCCAAATGAGAGAACCAAGG

GGAAGTGACATAGCAGGAACCTACTAGTACCCTTCAGGAACAAATAGGATGGATGACAAATAATCCACCTATCCCAGTA

Inact.6
GGAGAAATCTATAAAGATGGATAATCCTGGGATTAAATAAAATAGTAAGATGTATAGCCCTACCAGCATTCTGGAC
C G G G C G C G G

ATAAGACAAGGACCAAGGAACCCCTTTAGAGATTATGTAGACCGGTTCTATAAACTCTAAGAGGCTAACAAGCTTCA

Inact.7
CAGGATGTAAAAAATTGGATGACAGAAACCTTGTGGTCCAAAATGCAAACCCAGATTGTAAGAGTATTTTAAAGCA
C CC G G T

Inact.7
TTGGGACCAGCAGCTACACTAGAAGAAATGATGACAGCATGTCAGGGAGTGGGGGGACCCGGCCATAAGCAAGAGTT
C C C G

Inact.8
TTGGGTGAAGCCATGAGCCAAGTAACAAATCCAGCTACATAATGATGCAGAGAGGCAATTTTAGGAACCAAGAAAG
C G G G G G C G G C

Inact.9
CAATTTTAGGAACCAAGAAAG
C CC GC G

Inact.9
ACTGTTAAGTGTTCATTTGTGGCAAAGAAGGGCACAATAGCCAAAATTGCAGGGCCCCCTAGGAAGAGGGCTGTTGG
C C C CC GG C C CC G

Inact.10
TAGCCAAAATTGCAGGGCCCCCTAGGAAGAGGGCTGTTGG
CC GG C C CC G

AGATGTGGAAGGGAAGGACACCAAATGAAAGATTGCACTGAGAGACAGGCTAATTTTTTAGGGAAGATCTGGCCTTCC

From here no changes to native sequence (GP1) and (GP2)

TACAAGGGAAGGCCAGGGAATTTCTTCAGAGCAGACCAGAGCCAACAGCCCCACCAGAAGAGAGCTTCAGGTTTGGG

GAGGAGAAAACAACTCCCTCTCAGAAGCAGGAGCCGATAGACAAGGAAGTATCCTTTAACTTCCCTCAGATCACTC

From here codon optimization + inactivation (GP1)

Inact.11 or only inactivation (GP2)
ATAAGGATAGGGGGGCACTAAAGGAAGCTCTATTAGATACAGGAGCAGATGATA
G C C G C G

Inact.12
CAGTATTAGAAGAAATGAATTTGCCAGGAAATGGAACCAAAAATGATAGGGGCAATTGGAGGTTTATCAAAGTAA
G C G C C G G

Inact.12
GACAGTACGATCAGATACCTGTAGAAATCTGTGGACATAAAGCTATAGGTACAGTATTAGTAGGACCTACACCTGTCA
G C

Inact.13
ACATAATTGGAAGAAATCTGTTGACTCAGATTGGTTGTACTTTAAATTTCCCATAGTCTATTGAACTGTACCAG
C C C C C G C C C

Inact.14
TAAATTTAAAGCCAGGAATGGATGGCCCAAAAGTTAAGCAATGGCCATTGTAA
G G G G G C C G G

FIG. 2

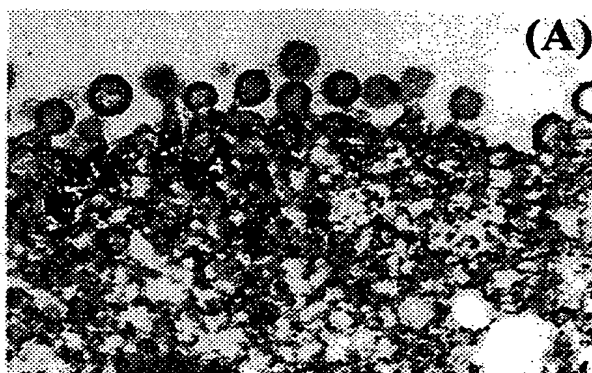


FIG. 3A

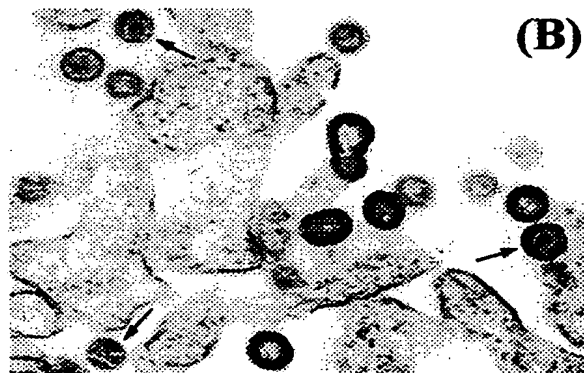


FIG. 3B

4 / 131

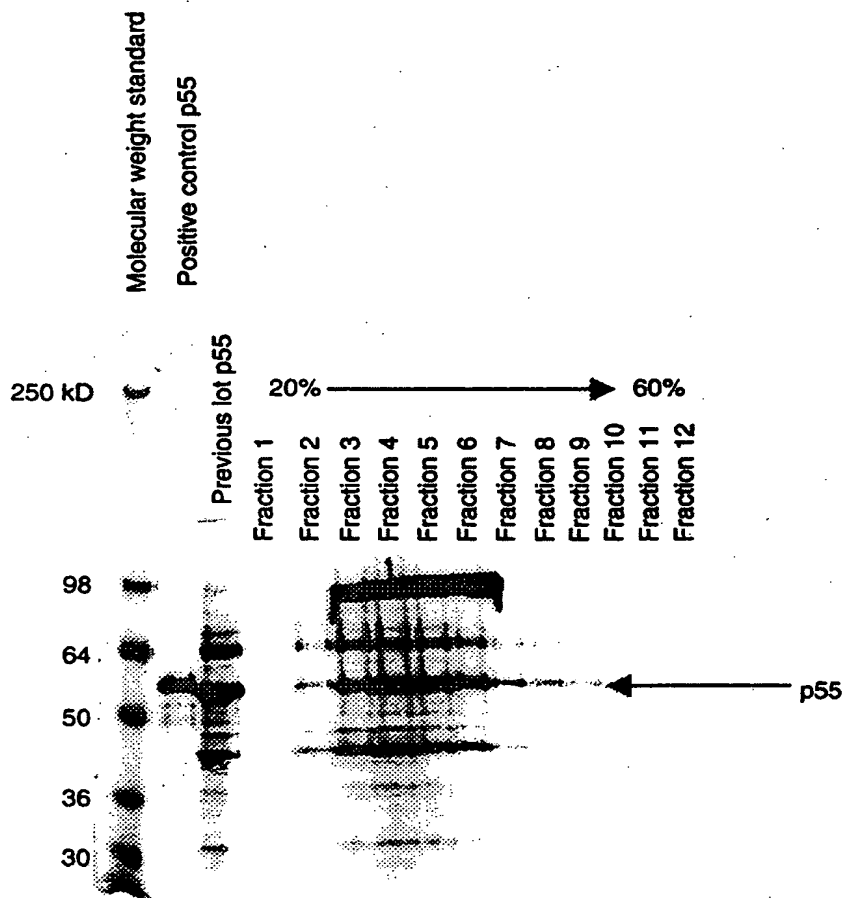


FIG. 4

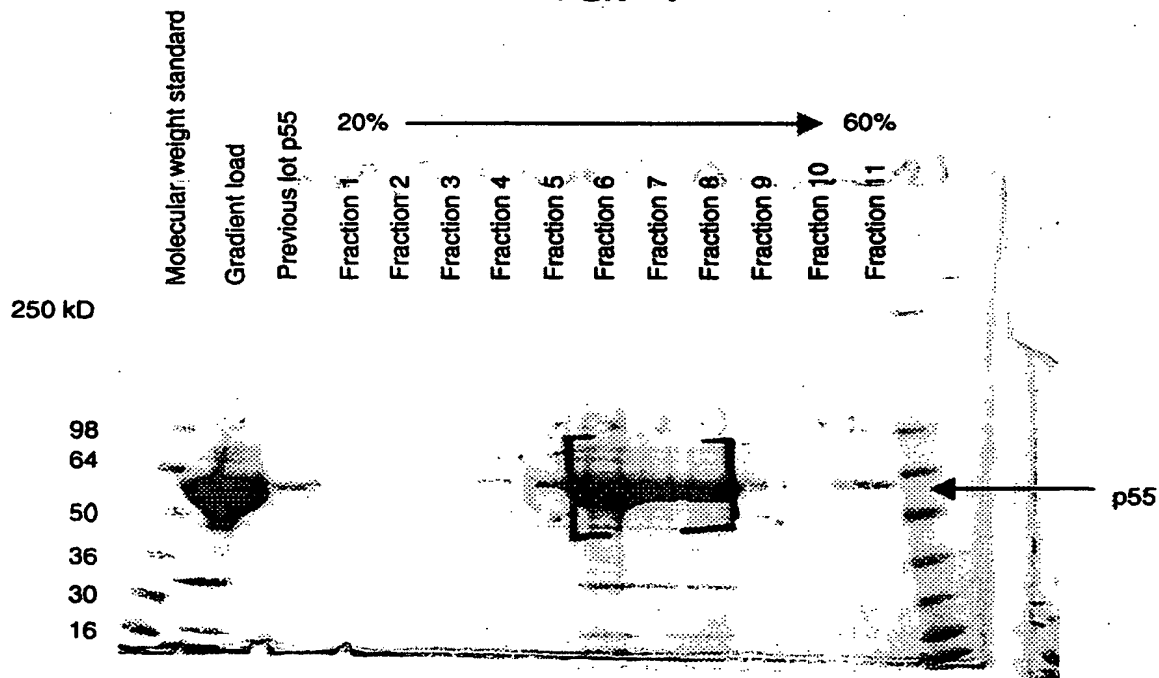


FIG. 5

5 / 131

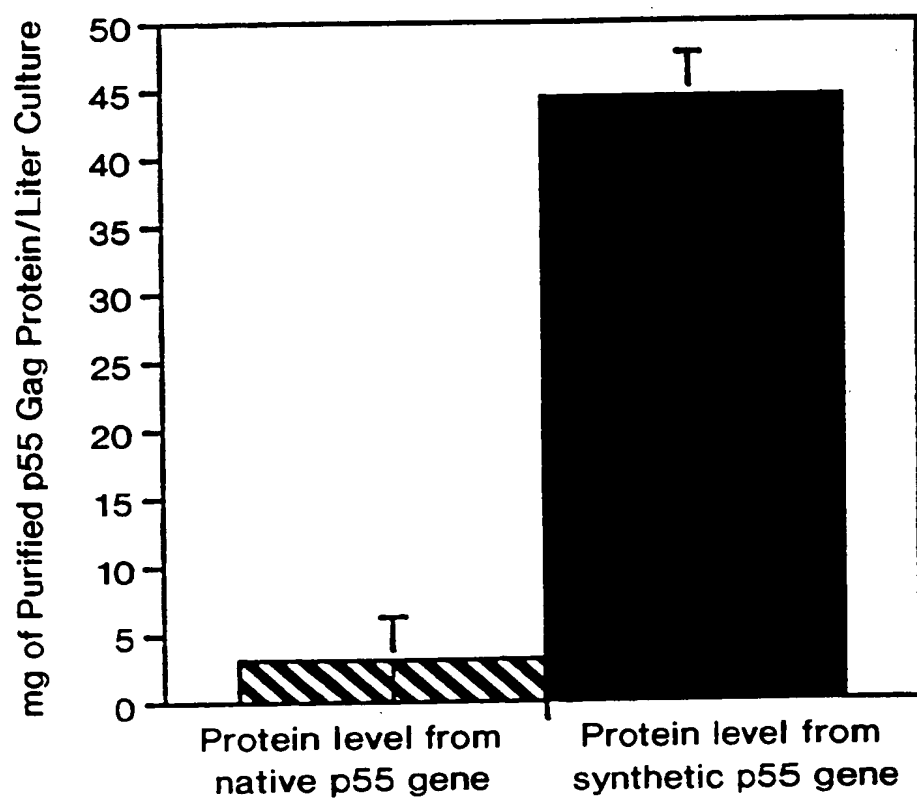


FIG. 6

6 / 131

GagPol.ModSF	1	ATGGGCGCCC	GCGCCAGCGT	GCTGAGCGGC	GCGGAGCTGG	ACAAGTGGGA	50
GagProt.ModS	1	ATGGGCGCCC	GCGCCAGCGT	GCTGAGCGGC	GCGGAGCTGG	ACAAGTGGGA	50
Gag.ModSF2	1	ATGGGCGCCC	GCGCCAGCGT	GCTGAGCGGC	GCGGAGCTGG	ACAAGTGGGA	50
	60	70	80	90	100		
GagPol.ModSF	51	GAAGATCCGC	CTGGCCCCG	GCGCAAGAA	GAAGTACAAG	CTGAAGCACA	100
GagProt.ModS	51	GAAGATCCGC	CTGGCCCCG	GCGCAAGAA	GAAGTACAAG	CTGAAGCACA	100
Gag.ModSF2	51	GAAGATCCGC	CTGGCCCCG	GCGCAAGAA	GAAGTACAAG	CTGAAGCACA	100
	110	120	130	140	150		
GagPol.ModSF	101	TCGTGTGGC	CAGCCGCGAG	CTGGAGCGCT	TCGCCGTGAA	CCCCGGCCTG	150
GagProt.ModS	101	TCGTGTGGC	CAGCCGCGAG	CTGGAGCGCT	TCGCCGTGAA	CCCCGGCCTG	150
Gag.ModSF2	101	TCGTGTGGC	CAGCCGCGAG	CTGGAGCGCT	TCGCCGTGAA	CCCCGGCCTG	150
	160	170	180	190	200		
GagPol.ModSF	151	CTGGAGACCA	GCGAGGGCTG	CGCCAGATC	CTGGGCCAGC	TGCAGCCCAG	200
GagProt.ModS	151	CTGGAGACCA	GCGAGGGCTG	CGCCAGATC	CTGGGCCAGC	TGCAGCCCAG	200
Gag.ModSF2	151	CTGGAGACCA	GCGAGGGCTG	CGCCAGATC	CTGGGCCAGC	TGCAGCCCAG	200
	210	220	230	240	250		
GagPol.ModSF	201	CCTGCAGACC	GGCAGCGAGG	AGCTGCGCAG	CCTGTACAAC	ACCGTGGCCA	250
GagProt.ModS	201	CCTGCAGACC	GGCAGCGAGG	AGCTGCGCAG	CCTGTACAAC	ACCGTGGCCA	250
Gag.ModSF2	201	CCTGCAGACC	GGCAGCGAGG	AGCTGCGCAG	CCTGTACAAC	ACCGTGGCCA	250
	260	270	280	290	300		
GagPol.ModSF	251	CCCTGTACTG	CGTGCACCAG	CGCATCGACG	TCAAAGGACAC	CAAGGAGGCC	300
GagProt.ModS	251	CCCTGTACTG	CGTGCACCAG	CGCATCGACG	TCAAAGGACAC	CAAGGAGGCC	300
Gag.ModSF2	251	CCCTGTACTG	CGTGCACCAG	CGCATCGACG	TCAAAGGACAC	CAAGGAGGCC	300
	310	320	330	340	350		
GagPol.ModSF	301	CTGGAGAAGA	TCGAGGAGGA	GCAGAACAAG	TCCAAGAAGA	AGGCCCAGCA	350
GagProt.ModS	301	CTGGAGAAGA	TCGAGGAGGA	GCAGAACAAG	TCCAAGAAGA	AGGCCCAGCA	350
Gag.ModSF2	301	CTGGAGAAGA	TCGAGGAGGA	GCAGAACAAG	TCCAAGAAGA	AGGCCCAGCA	350
	360	370	380	390	400		
GagPol.ModSF	351	GGCCGCCGCC	GCCGCCGGCA	CCGGCAACAG	CAGCCAGGTG	AGCCAGAACT	400
GagProt.ModS	351	GGCCGCCGCC	GCCGCCGGCA	CCGGCAACAG	CAGCCAGGTG	AGCCAGAACT	400
Gag.ModSF2	351	GGCCGCCGCC	GCCGCCGGCA	CCGGCAACAG	CAGCCAGGTG	AGCCAGAACT	400
	410	420	430	440	450		
GagPol.ModSF	401	ACCCCATCGT	GCAGAACCTG	CAGGGCCAGA	TGGTGCACCA	GGCCATCAGC	450
GagProt.ModS	401	ACCCCATCGT	GCAGAACCTG	CAGGGCCAGA	TGGTGCACCA	GGCCATCAGC	450
Gag.ModSF2	401	ACCCCATCGT	GCAGAACCTG	CAGGGCCAGA	TGGTGCACCA	GGCCATCAGC	450

FIG. 7A

7 / 131

GagPol.ModSF	451	CCCCGACCC	TGAACGCCCTG	GGTGAAGGTG	GTGGAGGAGG	AGGCCTTCAG	500
GagProt.ModS	451	CCCCGACCC	TGAACGCCCTG	GGTGAAGGTG	GTGGAGGAGG	AGGCCTTCAG	500
Gag.ModSF2	451	CCCCGACCC	TGAACGCCCTG	GGTGAAGGTG	GTGGAGGAGG	AGGCCTTCAG	500
GagPol.ModSF	501	CCCCGAGGTG	ATCCCCATGT	TCAGCGCCCT	GAGCGAGGCG	GCCACCCCCC	550
GagProt.ModS	501	CCCCGAGGTG	ATCCCCATGT	TCAGCGCCCT	GAGCGAGGCG	GCCACCCCCC	550
Gag.ModSF2	501	CCCCGAGGTG	ATCCCCATGT	TCAGCGCCCT	GAGCGAGGCG	GCCACCCCCC	550
GagPol.ModSF	551	AGGACCTGAA	CACGATGTTG	AACACCCGTG	GCGGCCACCA	GGCCGCCATG	600
GagProt.ModS	551	AGGACCTGAA	CACGATGTTG	AACACCCGTG	GCGGCCACCA	GGCCGCCATG	600
Gag.ModSF2	551	AGGACCTGAA	CACGATGTTG	AACACCCGTG	GCGGCCACCA	GGCCGCCATG	600
GagPol.ModSF	601	CAGATGCTGA	AGGAGACCAT	CAACGAGGAG	GCCGCCGAGT	GGGACCGCGT	650
GagProt.ModS	601	CAGATGCTGA	AGGAGACCAT	CAACGAGGAG	GCCGCCGAGT	GGGACCGCGT	650
Gag.ModSF2	601	CAGATGCTGA	AGGAGACCAT	CAACGAGGAG	GCCGCCGAGT	GGGACCGCGT	650
GagPol.ModSF	651	GCACCCCGTG	CACGCCGGCC	CCATCGCCCC	CGGCCAGATG	CGCGAGCCCC	700
GagProt.ModS	651	GCACCCCGTG	CACGCCGGCC	CCATCGCCCC	CGGCCAGATG	CGCGAGCCCC	700
Gag.ModSF2	651	GCACCCCGTG	CACGCCGGCC	CCATCGCCCC	CGGCCAGATG	CGCGAGCCCC	700
GagPol.ModSF	701	GCGGCAGCGA	CATCGCCGGC	ACCACACGCA	CCCTGCAGGA	GCAGATCGGC	750
GagProt.ModS	701	GCGGCAGCGA	CATCGCCGGC	ACCACACGCA	CCCTGCAGGA	GCAGATCGGC	750
Gag.ModSF2	701	GCGGCAGCGA	CATCGCCGGC	ACCACACGCA	CCCTGCAGGA	GCAGATCGGC	750
GagPol.ModSF	751	TGGATGACCA	ACAACCCCCC	CATCCCCCGT	GGCGAGATCT	ACAAGCGGTG	800
GagProt.ModS	751	TGGATGACCA	ACAACCCCCC	CATCCCCCGT	GGCGAGATCT	ACAAGCGGTG	800
Gag.ModSF2	751	TGGATGACCA	ACAACCCCCC	CATCCCCCGT	GGCGAGATCT	ACAAGCGGTG	800
GagPol.ModSF	801	GATCATCCTG	GGCCTGAACA	AGATCGTGCG	GATGTACAGC	CCCACACGCA	850
GagProt.ModS	801	GATCATCCTG	GGCCTGAACA	AGATCGTGCG	GATGTACAGC	CCCACACGCA	850
Gag.ModSF2	801	GATCATCCTG	GGCCTGAACA	AGATCGTGCG	GATGTACAGC	CCCACACGCA	850
GagPol.ModSF	851	TCCTGGACAT	CGGCCAGGGC	CCCAAGGAGC	CCTTCGCGCA	CTACGTGGAC	900
GagProt.ModS	851	TCCTGGACAT	CGGCCAGGGC	CCCAAGGAGC	CCTTCGCGCA	CTACGTGGAC	900
Gag.ModSF2	851	TCCTGGACAT	CGGCCAGGGC	CCCAAGGAGC	CCTTCGCGCA	CTACGTGGAC	900

FIG. 7B

8 / 131

FIG. 7C

GagPol.ModSF	901	CGCTTCTACA	910	AGACCCCTGCG	920	CGCTGAGCAG	930	GCCAGCCAGG	940	ACGTGAAGAA	950
GagProt.ModS	901	CGCTTCTACA		AGACCCCTGCG		CGCTGAGCAG		GCCAGCCAGG		ACGTGAAGAA	950
Gag.ModSF2	901	CGCTTCTACA	960	AGACCCCTGCG	970	CGCTGAGCAG	980	GCCAGCCAGG	990	ACGTGAAGAA	1000
GagPol.ModSF	951	CTGGATGACC		GAGACCCCTGC		TGGTGCAGAA		CGCCAACCCC		GA CTGCAAGA	1000
GagProt.ModS	951	CTGGATGACC		GAGACCCCTGC		TGGTGCAGAA		CGCCAACCCC		GA CTGCAAGA	1000
Gag.ModSF2	951	CTGGATGACC	1010	GAGACCCCTGC	1020	TGGTGCAGAA	1030	CGCCAACCCC	1040	GA CTGCAAGA	1050
GagPol.ModSF	1001	CCATCCTGAA		GGCTCTCGGC		CCCGCGGCCA		CCCTGGAGGA		GATGATGACC	1050
GagProt.ModS	1001	CCATCCTGAA		GGCTCTCGGC		CCCGCGGCCA		CCCTGGAGGA		GATGATGACC	1050
Gag.ModSF2	1001	CCATCCTGAA	1060	GGCTCTCGGC	1070	CCCGCGGCCA	1080	CCCTGGAGGA	1090	GATGATGACC	1100
GagPol.ModSF	1051	GCCTGCCAGG		GGCTGGGCGG		CCCCGGCCAC		AAGGCCCGCG		TGCTGGCCGA	1100
GagProt.ModS	1051	GCCTGCCAGG		GGCTGGGCGG		CCCCGGCCAC		AAGGCCCGCG		TGCTGGCCGA	1100
Gag.ModSF2	1051	GCCTGCCAGG	1110	GGCTGGGCGG	1120	CCCCGGCCAC	1130	AAGGCCCGCG	1140	TGCTGGCCGA	1150
GagPol.ModSF	1101	GGCGATGAGC		CAGGTGACGA		ACCCGGCGGAC		CATCATGATG		CAGCGCGGCA	1150
GagProt.ModS	1101	GGCGATGAGC		CAGGTGACGA		ACCCGGCGGAC		CATCATGATG		CAGCGCGGCA	1150
Gag.ModSF2	1101	GGCGATGAGC	1160	CAGGTGACGA	1170	ACCCGGCGGAC	1180	CATCATGATG	1190	CAGCGCGGCA	1200
GagPol.ModSF	1151	ACTTCCGCAA		CCAGCGGAAG		ACCGTCAAGT		GCTTCAACTG		CGGCAAGGAG	1200
GagProt.ModS	1151	ACTTCCGCAA		CCAGCGGAAG		ACCGTCAAGT		GCTTCAACTG		CGGCAAGGAG	1200
Gag.ModSF2	1151	ACTTCCGCAA	1210	CCAGCGGAAG	1220	ACCGTCAAGT	1230	GCTTCAACTG	1240	CGGCAAGGAG	1250
GagPol.ModSF	1201	GGCCACACCG		CCAGGAACTG		CCGCGCCCCC		CGCAAGAAGG		GCTGCTGGCG	1250
GagProt.ModS	1201	GGCCACACCG		CCAGGAACTG		CCGCGCCCCC		CGCAAGAAGG		GCTGCTGGCG	1250
Gag.ModSF2	1201	GGCCACACCG	1260	CCAGGAACTG	1270	CCGCGCCCCC	1280	CGCAAGAAGG	1290	GCTGCTGGCG	1300
GagPol.ModSF	1251	CTGCGGCCGC		GAAGGACACC		AAATGAAAGA		TTGCACTGAG		AGACAGGCTA	1300
GagProt.ModS	1251	CTGCGGCCGC		GAAGGACACC		AAATGAAAGA		TTGCACTGAG		AGACAGGCTA	1300
Gag.ModSF2	1251	CTGCGGCCGC	1310	GAGGGCCACC	1320	AGATGAAGGA	1330	CTGCACCGAG	1340	CGCCAGGCCA	1350
GagPol.ModSF	1301	ATTTTCTAGG		GAAGATCTGG		CCTTCCTACA		AGGGAAGGCC		AGGGAATTTT	1350
GagProt.ModS	1301	ATTTTCTAGG		GAAGATCTGG		CCTTCCTACA		AGGGAAGGCC		AGGGAATTTT	1350
Gag.ModSF2	1301	ATTTTCTAGG	1301	CAAGATCTGG	1301	CCCAGCTACA	1301	AGGCGCGCCC	1301	CGGCAACTTC	1350

9 / 131

GagPol.ModSF	1351	CTTCAGAGCA	1360	1370	1380	1390	1400
GagProt.ModS	1351	CTTCAGAGCA	GACCAGAGCC	AACAGCCCCA	CCAGAAGAGA	GCTTCAGGTT	1400
Gag.ModSF2	1351	CTGCAGAGCC	1410	1420	1430	1440	1450
GagPol.ModSF	1401	TGGGGAGGAG	AAAACAACTC	CCTCTCAGAA	GCAGGAGCCG	ATAGACAAGG	1450
GagProt.ModS	1401	TGGGGAGGAG	AAAACAACTC	CCTCTCAGAA	GCAGGAGCCG	ATAGACAAGG	1450
Gag.ModSF2	1401	CGGCGAGGAG	1460	1470	1480	1490	1500
GagPol.ModSF	1451	AACGTGTATCC	TTTAACTTCC	CTCAGATCAC	TCTTTGGCAA	CGACCCCTCG	1500
GagProt.ModS	1451	AACGTGTATCC	TTTAACTTCC	CTCAGATCAC	TCTTTGGCAA	CGACCCCTCG	1500
Gag.ModSF2	1451	AGCTGTATCC	1510	1520	1530	1540	1550
GagPol.ModSF	1501	TCACAGTAAG	GATCGGCGGC	CAGCTCAAGG	AGGCGCTGCT	CGACACCGGC	1550
GagProt.ModS	1501	TCACAGTAAG	GATCGGCGGC	CAGCTCAAGG	AGGCGCTGCT	CGACACCGGC	1550
Gag.ModSF2	1501	AGCCAGTAA	1560	1570	1580	1590	1600
GagPol.ModSF	1551	GCCGACGACA	CCGTGCTGGA	GGAGATGAAC	CTGCCCGGCA	AGTGAAGCC	1600
GagProt.ModS	1551	GCCGACGACA	CCGTGCTGGA	GGAGATGAAC	CTGCCCGGCA	AGTGAAGCC	1600
Gag.ModSF2	1551	1600
GagPol.ModSF	1601	CAAGATGATC	1610	1620	1630	1640	1650
GagProt.ModS	1601	CAAGATGATC	GGCGGGATCG	GGGGCTTCAT	CAAGGTGCGG	CAGTACGACC	1650
Gag.ModSF2	1601	1650
GagPol.ModSF	1651	AGATCCCCGT	1660	1670	1680	1690	1700
GagProt.ModS	1651	AGATCCCCGT	GGAGATCTGC	GGCCACAAGG	CCATCGGCAC	CGTGTGGTG	1700
Gag.ModSF2	1651	1700
GagPol.ModSF	1701	GGCCCCACCC	1710	1720	1730	1740	1750
GagProt.ModS	1701	GGCCCCACCC	CCGTGAACAT	CATCGGCCGC	AACCTGCTGA	CCCAGATCGG	1750
Gag.ModSF2	1701	1750
GagPol.ModSF	1751	CTGCACCCCTG	1760	1770	1780	1790	1800
GagProt.ModS	1751	CTGCACCCCTG	AACCTTCCCCA	TCAGCCCCCAT	CGAGACGGTG	CCCGTGAAGC	1800
Gag.ModSF2	1751	1800

FIG. 7D

10/ 131

GagPol.ModSF	1801	1810	1820	1830	1840	1850
GagPol.ModSF	1801	TGAAGCCGGG	GATGGACGGC	CCCAAGGTCA	AGCAGTGGCC	CCTGACCGAG
GagProt.ModS	1801	TGAAGCCGGG	GATGGACGGC	CCCAAGGTCA	AGCAGTGGCC	CCTGTAA...
Gag.ModSF2	1801
	1860	1870	1880	1890	1900	
GagPol.ModSF	1851	GAGAAGATCA	AGGCCCTGGT	GGAGATCTGC	ACCGAGATGG	AGAAGGAGGG
GagProt.ModS	1851
Gag.ModSF2	1851
	1910	1920	1930	1940	1950	
GagPol.ModSF	1901	CAAGATCAGC	AAGATCGGCC	CCGAGAACCC	CTACAACACC	CCCGTGTTCG
GagProt.ModS	1901
Gag.ModSF2	1901
	1960	1970	1980	1990	2000	
GagPol.ModSF	1951	CCATCAAGAA	GAAGGACAGC	ACCAAGTGSC	GCAAGCTGGT	GGACTTCCGC
GagProt.ModS	1951
Gag.ModSF2	1951
	2010	2020	2030	2040	2050	
GagPol.ModSF	2001	GAGCTGAACA	AGCGCACCCA	GGACTTCTGG	GAGGTGCAGC	TGGGCATCCC
GagProt.ModS	2001
Gag.ModSF2	2001
	2060	2070	2080	2090	2100	
GagPol.ModSF	2051	CCACCCCGCC	GGCCTGAAGA	AGAAGAAGAG	CGTGACCCGTG	CTGGACGTGG
GagProt.ModS	2051
Gag.ModSF2	2051
	2110	2120	2130	2140	2150	
GagPol.ModSF	2101	GCGACGCCTA	CTTCAGCGTG	CCCCTGGACA	AGGACTTCCG	CAAGTACACC
GagProt.ModS	2101
Gag.ModSF2	2101
	2160	2170	2180	2190	2200	
GagPol.ModSF	2151	GCCTTCACCA	TCCCCAGCAT	CAACAACGAG	ACCCCCGGCA	TCCGCTACCA
GagProt.ModS	2151
Gag.ModSF2	2151
	2210	2220	2230	2240	2250	
GagPol.ModSF	2201	GTACAACGTG	CTGCCCCCAGG	GCTGGAAGGG	CAGCCCCCGCC	ATCTTCCAGA
GagProt.ModS	2201
Gag.ModSF2	2201

FIG. 7E

11 / 131

GagPol.ModSF 2251	2260	2270	2280	2290	2300
	GCAGCATGAC	CAAGATCCTG	GAGCCCTTCC	GCAAGCAGAA	CCCCGACATC
GagProt.Mods 2251					2300
					2300
Gag.ModSF2 2251					2300
	2310	2320	2330	2340	2350
GagPol.ModSF 2301	GTGATCTACC	AGTACATGGA	CGACCTGTAC	GTGGGCAGCG	ACCTGGAGAT
GagProt.Mods 2301					2350
Gag.ModSF2 2301					2350
	2360	2370	2380	2390	2400
GagPol.ModSF 2351	CGGCCAGCAC	CGCACCAAGA	TCGAGGAGCT	GCGCCAGCAC	CTGCTGCGCT
GagProt.Mods 2351					2400
Gag.ModSF2 2351					2400
	2410	2420	2430	2440	2450
GagPol.ModSF 2401	GGGGCTTCAC	CACCCCCGAC	AAGAAGCACC	AGAAGGAGCC	CCCCCTTCCTG
GagProt.Mods 2401					2450
Gag.ModSF2 2401					2450
	2460	2470	2480	2490	2500
GagPol.ModSF 2451	TGGATGGCT	ACGAGCTGCA	CCCCGACAAG	TGGACCGTGC	AGCCCCATCAT
GagProt.Mods 2451					2500
Gag.ModSF2 2451					2500
	2510	2520	2530	2540	2550
GagPol.ModSF 2501	GCTGCCCCGAG	AAGGACAGCT	GGACCGTGAA	CGACATCCAG	AAGCTGGTGG
GagProt.Mods 2501					2550
Gag.ModSF2 2501					2550
	2560	2570	2580	2590	2600
GagPol.ModSF 2551	GCAAGCTGAA	CTGGGCCAGC	CAGATCTACG	CCGGCATCAA	GGTGAAGCAG
GagProt.Mods 2551					2600
Gag.ModSF2 2551					2600
	2610	2620	2630	2640	2650
GagPol.ModSF 2601	CTGTGCAAGC	TGCTGGCGGG	CACCAAGGCC	CTGACCGAGG	TGATCCCCCT
GagProt.Mods 2601					2650
Gag.ModSF2 2601					2650
	2660	2670	2680	2690	2700
GagPol.ModSF 2651	GACCGAGGAG	GCCGAGCTGG	AGCTGGCCGA	GAACCGCGAG	ATCCTGAAGG
GagProt.Mods 2651					2700
Gag.ModSF2 2651					2700

FIG. 7F

12 / 131

GagPol.ModSF 2701	2710	2720	2730	2740	2750
GagProt.Mods 2701	AGCCCGTGCA	CGAGGTGTAC	TACGACCCCA	GCAAGGACCT	GGTGGCCGAG
Gag.ModSF2 2701
GagPol.ModSF 2751	2760	2770	2780	2790	2800
GagProt.Mods 2751	ATCCAGAAGC	AGGGCCAGGG	CCAGTGGACC	TACCAGATCT	ACCAGGAGCC
Gag.ModSF2 2751
GagPol.ModSF 2801	2810	2820	2830	2840	2850
GagProt.Mods 2801	CTTCAAGAAC	CTGAAGACCG	GCAAGTACGC	CCGCATGCGC	GGCGCCACCA
Gag.ModSF2 2801
GagPol.ModSF 2851	2860	2870	2880	2890	2900
GagProt.Mods 2851	CCAACGACGT	GAAGCAGCTG	ACCGAGGCCG	TGCAGAAGGT	GAGCACCCGAG
Gag.ModSF2 2851
GagPol.ModSF 2901	2910	2920	2930	2940	2950
GagProt.Mods 2901	AGCATCGTGA	TCTGGGGCAA	GATCCCCAAG	TTCAAGCTGC	CCATCCAGAA
Gag.ModSF2 2901
GagPol.ModSF 2951	2960	2970	2980	2990	3000
GagProt.Mods 2951	GGAGACCTGG	GAGGCCTGGT	GGATGGAGTA	CTGGCAGGCC	ACCTGGATCC
Gag.ModSF2 2951
GagPol.ModSF 3001	3010	3020	3030	3040	3050
GagProt.Mods 3001	CCGAGTGGGA	GTTTCGTGAAC	ACCCCCCCCC	TGGTGAAGCT	GTGGTACCAG
Gag.ModSF2 3001
GagPol.ModSF 3051	3060	3070	3080	3090	3100
GagProt.Mods 3051	CTGGAGAAGG	AGCCCCATCGT	GGGCGCCGAG	ACCTTCTACG	TGGACGGCGC
Gag.ModSF2 3051
GagPol.ModSF 3101	3110	3120	3130	3140	3150
GagProt.Mods 3101	CGCCCAACCGC	GAGACCAAGC	TGGGCAAGGC	CGGCTACGTG	ACCGACCGCG
Gag.ModSF2 3101

FIG. 7G

13 / 131

GagPol.ModSF	3151	3160	3170	3180	3190	3200
GagProt.ModS	3151	GGTGGTGAGC	ATCGCCGACA	CCACCAACCA	GAAGACCGAG	3200
Gag.ModSF2	3151	3200
		3210	3220	3230	3240	3250
GagPol.ModSF	3201	CTGCAGGCCA	TCCACCTGSC	CCTGCAGGAC	AGCGGCTGG	AGGTGAACAT
GagProt.ModS	3201	3250
Gag.ModSF2	3201	3250
		3260	3270	3280	3290	3300
GagPol.ModSF	3251	CGTGACCGAC	AGCCAGTACG	CCCTGGGCAT	CATCCAGGCC	CAGCCCGACA
GagProt.ModS	3251	3300
Gag.ModSF2	3251	3300
		3310	3320	3330	3340	3350
GagPol.ModSF	3301	AGAGCGAGAG	CGAGCTGGTG	AGCCAGATCA	TCGAGCAGCT	GATCAAGAAG
GagProt.ModS	3301	3350
Gag.ModSF2	3301	3350
		3360	3370	3380	3390	3400
GagPol.ModSF	3351	GAGAAGGTGT	ACCTGGCCTG	GGTGCCCGCC	CACAAGGGCA	TCGGCGGGCAA
GagProt.ModS	3351	3400
Gag.ModSF2	3351	3400
		3410	3420	3430	3440	3450
GagPol.ModSF	3401	CGAGCAGGTG	GACAAGCTGG	TGAGCGCCGG	CATCCGCAAG	GTGCTGTTCC
GagProt.ModS	3401	3450
Gag.ModSF2	3401	3450
		3460	3470	3480	3490	3500
GagPol.ModSF	3451	TGAACGGCAT	CGACNAGGCC	CAGGAGGAGC	ACGAGAAGTA	CCACAGCAAC
GagProt.ModS	3451	3500
Gag.ModSF2	3451	3500
		3510	3520	3530	3540	3550
GagPol.ModSF	3501	TGGCGCGCCA	TGGCCAGCGA	CTTCAACCTG	CCCCCGTGG	TGGCCAAGGA
GagProt.ModS	3501	3550
Gag.ModSF2	3501	3550
		3560	3570	3580	3590	3600
GagPol.ModSF	3551	GATCGTGGCC	AGCTGCGACA	AGTGCCAGCT	GAAGGGCGAG	GCCATGCACG
GagProt.ModS	3551	3600
Gag.ModSF2	3551	3600

FIG. 7H

14 / 131

GagPol.ModSF 3601	3610	3620	3630	3640	3650
GagProt.Mods 3601	GCCAGGTGGA	CTGCAGCCCC	GGCATCTGGC	AGCTGGACTG	CACCCACCTG
Gag.ModSF2 3601
GagPol.ModSF 3651	3660	3670	3680	3690	3700
GagProt.Mods 3651	GAGGGCAAGA	TCATCCTGGT	GGCCGTGCAC	GTGGCCAGCG	GCTACATCGA
Gag.ModSF2 3651
GagPol.ModSF 3701	3710	3720	3730	3740	3750
GagProt.Mods 3701	GGCCGAGGTG	ATCCCGCGCG	AGACCGGCCA	GGAGACCGCC	TACTTCCTGC
Gag.ModSF2 3701
GagPol.ModSF 3751	3760	3770	3780	3790	3800
GagProt.Mods 3751	TGAAGCTGGC	CGGCCGCTGG	CCCGTGAAGA	CCATCCACAC	CGACAACGGC
Gag.ModSF2 3751
GagPol.ModSF 3801	3810	3820	3830	3840	3850
GagProt.Mods 3801	AGCAACTTCA	CCAGCACCAC	CGTGAAGGCC	GCCTGCTGGT	GGGCCGGGCAT
Gag.ModSF2 3801
GagPol.ModSF 3851	3860	3870	3880	3890	3900
GagProt.Mods 3851	CAAGCAGGAG	TTCGGCATCC	CCTACAACCC	CCAGAGCCAG	GGCGTGGTGG
Gag.ModSF2 3851
GagPol.ModSF 3901	3910	3920	3930	3940	3950
GagProt.Mods 3901	AGAGCATGAA	CAACGAGCTG	AAGAAGATCA	TCGGCCAGGT	GCGCGACCAG
Gag.ModSF2 3901
GagPol.ModSF 3951	3960	3970	3980	3990	4000
GagProt.Mods 3951	GCCGAGCACC	TGAAGACCGC	CGTGCAGATG	GCCGTGTTCA	TCCACAACCT
Gag.ModSF2 3951
GagPol.ModSF 4001	4010	4020	4030	4040	4050
GagProt.Mods 4001	CAAGCGCAAG	GGCGGCATCG	GCGGCTACAG	CGCCGGCGAG	CGCATCGTGG
Gag.ModSF2 4001

FIG. 7I

15 / 131

GagPol.ModSF	4051	ACATCATCGC	4060	4070	4080	4090	4100
GagProt.ModS	4051	CACCGACATC	CAGACCAAGG	AGCTGCAGAA	GCAGATCACC	4100
Gag.ModSF2	4051	4100
GagPol.ModSF	4101	AAGATCCAGA	4110	4120	4130	4140	4150
GagProt.ModS	4101	ACTTCCGCGT	GTACTACCGC	GACAAACAAGG	ACCCCTGTG	4150
Gag.ModSF2	4101	4150
GagPol.ModSF	4151	GAAGGGCCCC	4160	4170	4180	4190	4200
GagProt.ModS	4151	GCCAAAGCTGC	TGTGGAAGGG	CGAGGGCGCC	GTGGTGATCC	4200
Gag.ModSF2	4151	4200
GagPol.ModSF	4201	AGGACAACAG	4210	4220	4230	4240	4250
GagProt.ModS	4201	CGACATCAAG	GTGGTGCCCC	GCCGCAAGGC	CAAGATCATC	4250
Gag.ModSF2	4201	4250
GagPol.ModSF	4251	CGCGACTACG	4260	4270	4280	4290	4300
GagProt.ModS	4251	GCAAGCAGAT	GGCCGGCGGAC	GACTGCGTGG	CCAGCCGCCA	4300
Gag.ModSF2	4251	4300
GagPol.ModSF	4301	GGACGAGGAC	4310	4320	4330	4340	4350
GagProt.ModS	4301	TAG.....	4350
Gag.ModSF2	4301	4350

FIG. 7J

16 / 131

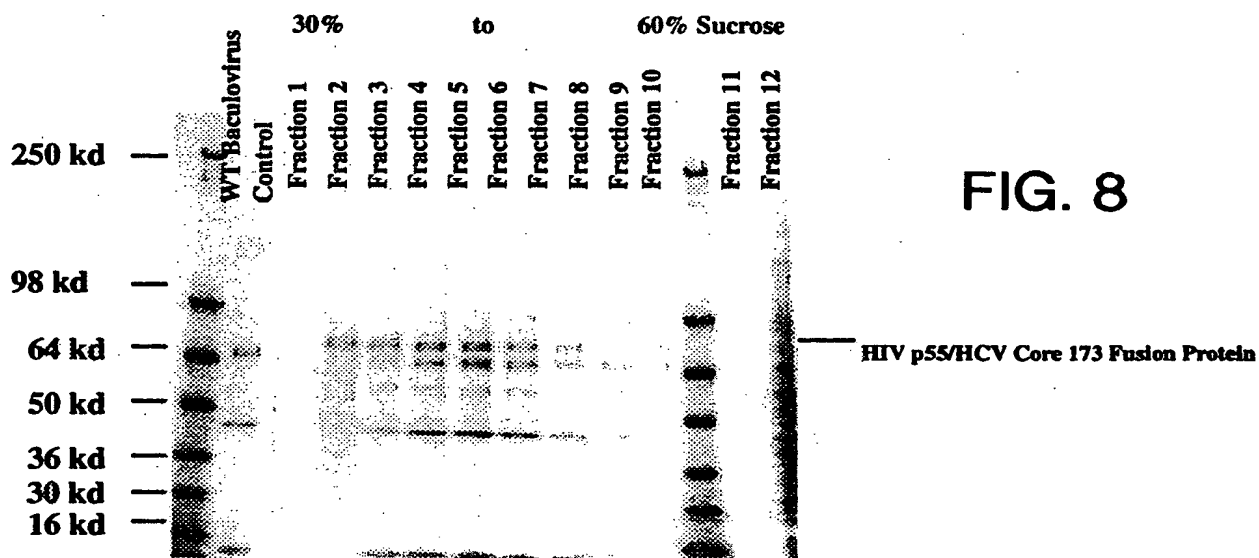


FIG. 8

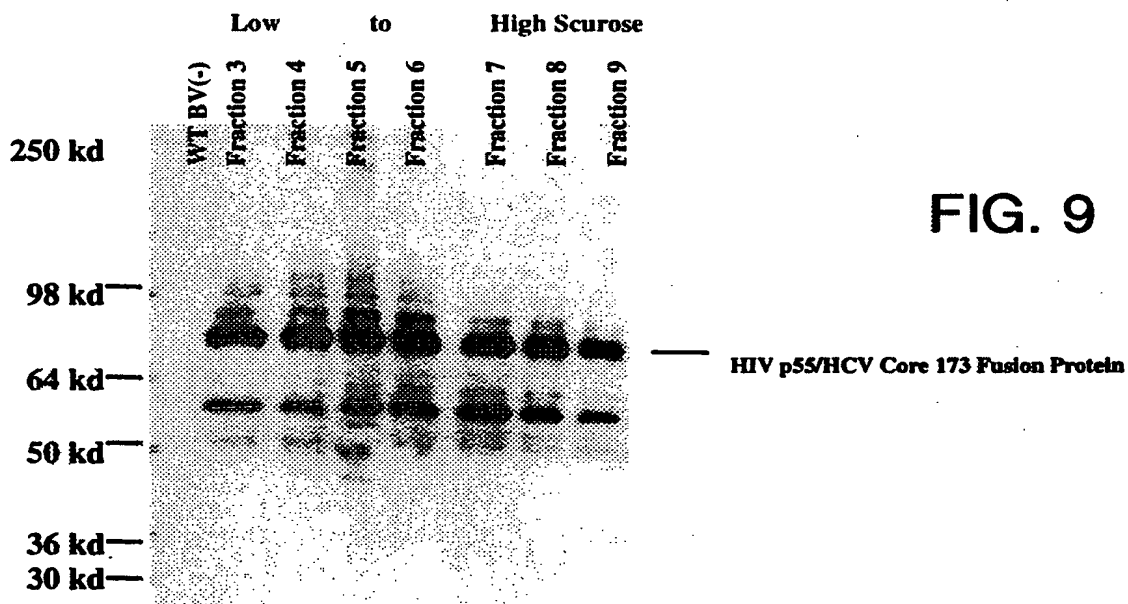


FIG. 9

17 / 131

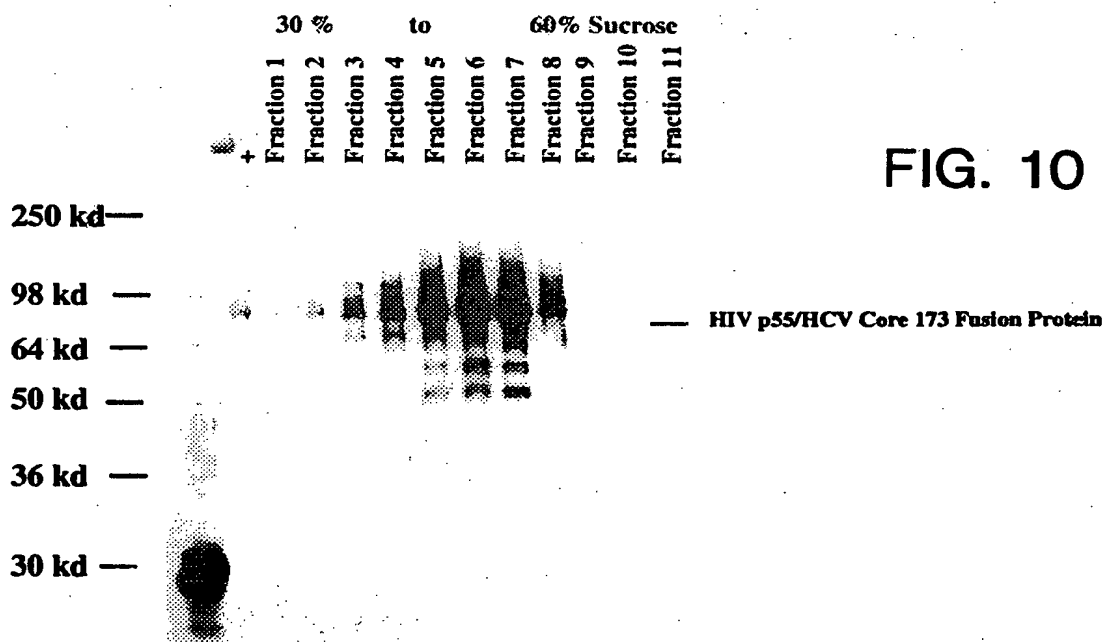


FIG. 10

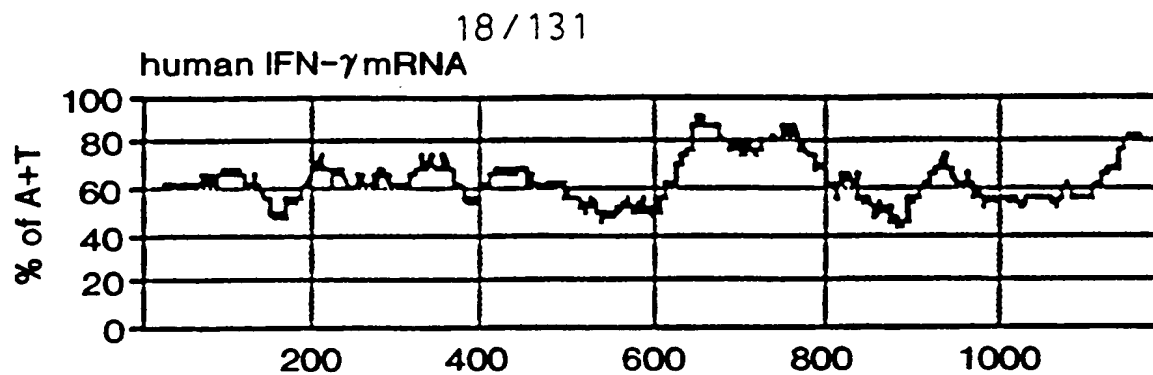


FIG. 11A

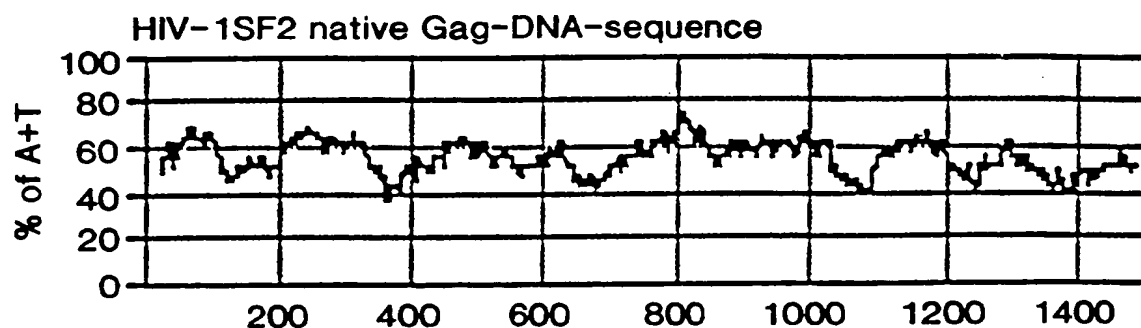


FIG. 11B

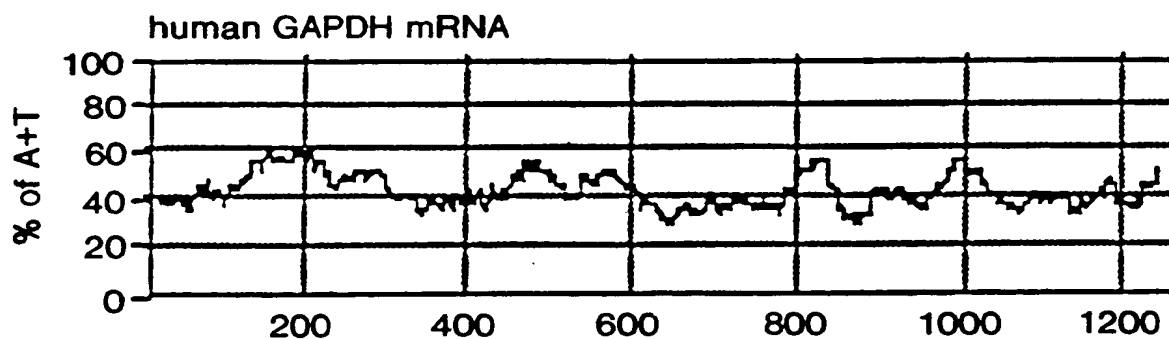


FIG. 11C

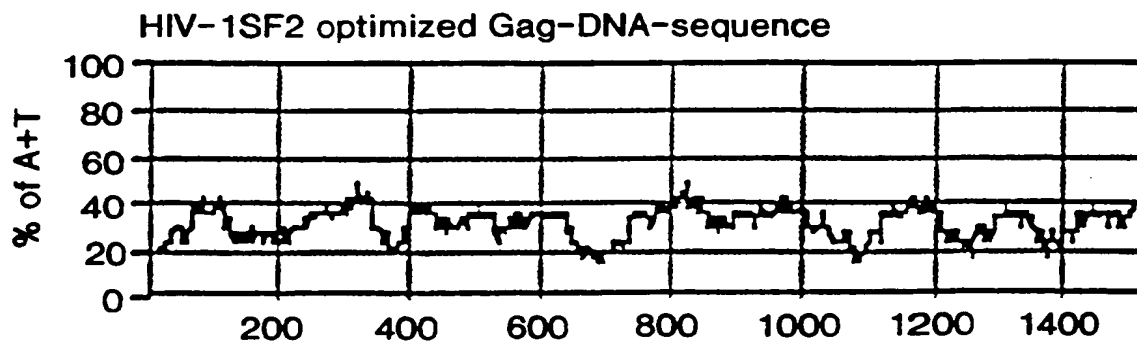


FIG. 11D

SUBSTITUTE SHEET (RULE 26)

native HIV-1SF2 gag-polymerase

ATGGGTGCGAGAGCGTCGGTATTAAAGCGGGGAGAAATTAGATAAATGGGAAAAAATTCGGTTAAGGCCAGGGGGAAAG

Inact.1
 AAAAAATATAAGTTAAAAACATATAGTATGGGCAAGCAGGGAGCTAGAACGATTCCGAGTCAATCCTGGCCTGTTAGAA
 G G C C G C C

Inact.2
 ACATCAGAAAGGCTGCAGACAAATATTGGGACAGCTACAGCCATCCCTTCAGACAGGATCAGAAAGAACTTTAGATCATTA
 G G C C

Inact.3
 TATAATACAGTAGCAACCCCTCTATTGTGTACATCAAAAGGATAGATGTAAGAAACACCAAGGAAGCTTTAGAGAAAGATA
 C GC C C G

Inact.4
 GAGGAAGAGCAAAACAAAGTAAGAAAAAGGCACAGCAAGCAGCAGCTGCAGCTGGCACAGGAAACAGCAGCCAGGTC
 GTCC G C G

AGCCAAAAATTACCCCTATAGTGCAGAACCTACAGGGGCAATGGTACATCAGGCCATATCACCTAGAACTTTAAATGCA

TGGGTAAGAAGTAGTAAGAAAAAGGCTTTCAGCCCAGAAGTAATACCCATGTTTTCAGCATTATCAGAAGGAGCCACC

Inact.5
 CCACAAAGATTTAACACCCATGCTAAACACACAGTGGGGGGACATCAAGCAGCCCATGCAATGTTAAAAAGAGACTATCAAT
 G CC G G T G C

GAGGAAGCTCGAGAATGGGATAGAGTGCATCCAGTGCATGCAAGGGCTATTGCACCAGGCCAAATGAGAGAACCAAGG

GGAAGTGACATAGCAGGAACTACTAGTACCCCTTCAGGAACAAATAGGATGGATGACAAATAATCCACCTATCCCAGTA

Inact.6
 GGAGAAATCTATAAAAGATGGATAATCCTGGGATTAAATAAAATAGTAAGAAATGATAGCCCTACCAGCATTCTGGAC
 G C G G G C G C G G

ATAAGACAAAGGACCAAGGAACCCCTTTAGAGATTATGTAGACCGGTTCTATAAAACTCTAAGAGCCGGAACAAGCTTCA

FIG. 12A

SUBSTITUTE SHEET (RULE 26)

AGATATGTACAGAAATGGAAAAGGAAGGGGAAAATTTCAAAAATTTGGGCCTGAAAATCCATACATACTCCAGTATTTG
CTATAAAGAAAAAGACAGTACTAAATGGAGAAAACCTAGTAGATTTTCAAGAACTTAATAAAGAACTCAAGACTTCT
GGGAAGTTTCAAGTTAGGAATACCAACCCCGAGGTTTAAAAAGAAAATCAGTAACAGTATGGATGTGGTGATG
CATACTTTTCAAGTTTCCCTTAGATAAAGACTTTAGAAAAGTATATGCAATTTACCAATACCTAGTATAAACAATGAGACAC
CAGGGATTAGATATCAGTACAATGTGCTGCCAGGGATGGAAGGATCACAGCAATATTTCCAAAGTAGCATGACAA
AAATCTTAGAGCCTTTTAGAAAAACAGAAATCCAGACATAGTTATCTATCAATACATGGATGATTTGTATGTAGGATCTG
ACTTAGAAATAGGCGAGCATAGAAACAAAATAGAGGAACTGAGACGATCTGTTGAGGTGGGGATTTTACCACACCCAG
ACAAAAACATCAGAAAGAACCTCCATTCCTTTGGATGGTTATGAACTCCATCCTGATAAATGGACAGTACAGCCCTA
TAATGCTGCCAGAAAAAGACAGCTGGACTGTCAATGACATACAGAAAGTTAGTGGGAAAATTTGAATTTGGGCAAGTCAGA
TTTATGCAGGGATTAAAGTAAAGCAGTTATGTAAAATCCTTAGAGGAACCAAGCACTAACAGAACTAATACCACTAA
CAGAAAGCAGAGCTAGAACTGGCAGAAAACAGGGAGATTCTAAAAGAACCAAGTACATGAAGTATATTATGACCCAT
CAAAAGACTTAGTAGCAAAATACAGAAAGCAGGGGCAAGGCCAATGGACATATCAAAATTTATCAAGAGCCATTTAAAA
ATCTGAAAACAGGAAAGTATGCAAGGATGAGGGTGCCCACTAATGATGTAAAACAGTTAAACAGAGGCGAGTGCAAA
AAGTATCCACAGAAAGCATAGTAATATGGGGAAGATTCTTAATTTAAACTACCCATACAAAAGGAAACATGGGAAG
CATGGTGGATGGAGTATTTGGCAAGCTACCTGGATTCCTGAGTGGGAGTTTGTCAATACCCCTCCCTTAGTGAATTTAT
GGTACCAGTTAGAGAAAGAACCCATAGTAGGAGCAGAACTTTCTATGTAGATGGGCGAGTAAATAGGGAGACTAAAT
TAGGAAAACAGGATATGTTACTGACAGAGGAAGACAAAAGTTGTCTCCATAGCTGACACAAACAATCAGAAGACTG
AATTACAAGCAATTCATCTAGCTTTGCAGGATTCGGGATTAGAAAGTAAACATAGTAACAGACTCACAATATGCATTAG
GAATCATTCAAAGCAACCAAGATAAGAGTGAATCAGAGTTAGTCAGTCAATATAGAGCAGTTAATAAAGGAA
AGGTCTACCTGGCATGGGTACCAAGCACAAAGGAATTTGGAGGAAATGAACAAGTAGATAAATAGTCAGTGTGGAA
TCAGGAAAGTACTATTTTGAATGGAATAGATAAGGCCCAAGAAACATGAGAAATATCAGAAATTTGGAGAGCAA
TGGCTAGTGATTTTAACTGCCACCTGTAGTAGCAAAAGAAATAGTAGCCAGCTGTGATAATGTCAAGTAAAGGAG
AAGCCATGCATGGACAAGTAGACTGTAGTCCAGGAATATGGCAACTAGATTGTACACATCTAGAAGGAAAAATTTATCC
TGGTAGCAGTTCATGTAGCCAGTGGATATATAGAAAGCAAGATTATCCAGCAGAGACAGGCGAGGAAACAGCATATT
TTCTCTTAAAAATTAGCAGGAAGATGGCCAGTAAAAACAATACATACAGCAATGGCAGCAATTTCCAGTACTACGG
TTAAGGCCGCCCTGTTGGTGGGCGAGGATCAAGCAGGAATTTGGCATTTCCCTACAATCCCCAAAGTCAAGGAGTAGTAG
AATCTATGAATATGAATTAAGAAAATTTATAGGACAGGTAAGAGATCAGGTGAACACCTTAAGACAGCAGTACAAA
TGCGCAGTATTCATCCACAATTTTAAAGAAAAGGGGGATTGGGGGATACAGTGCAGGGGAAAGAAATAGTAGACATAA
TAGCAACAGACATACAACTAAAGAACTACAAAAGCAATTTACAAAATTTTGGGTTTATTACAGGGACA
ACAAAGATCCCTTTGGAAAGGACCAAGCAAGCTTCTCTGGAAAGGTGAAGGGGCGAGTAGTAATAAAGATAAATAGTG
ACATAAAAGTAGTGCCCAAGAAAGCAAAAATCATTAGGGATTATGGAAAACAGATGGCAGGTGATGATTGTGTGG
CAAGTAGACAGGATGAGGATTAG

FIG. 12C

22 / 131

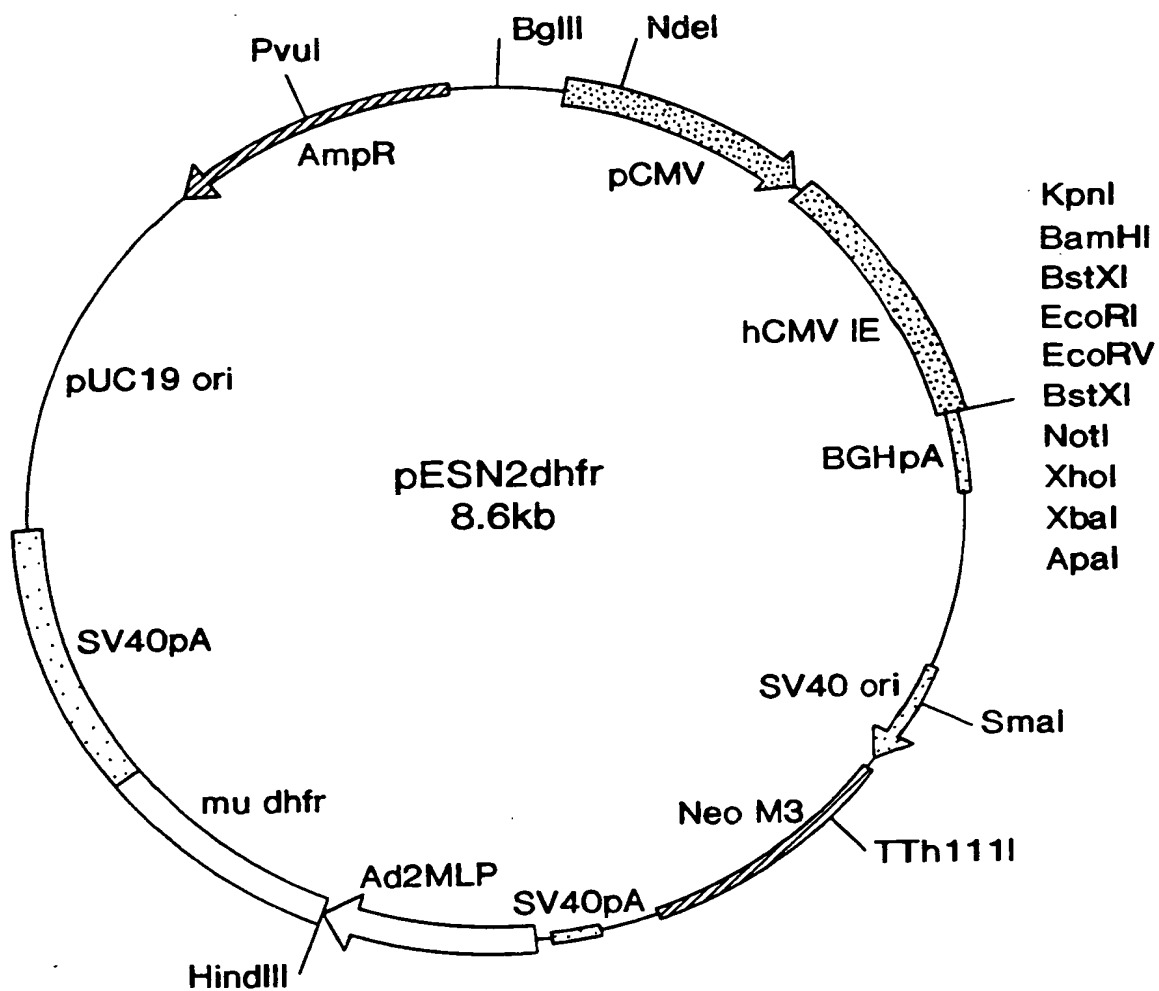


FIG. 13A

23 / 131

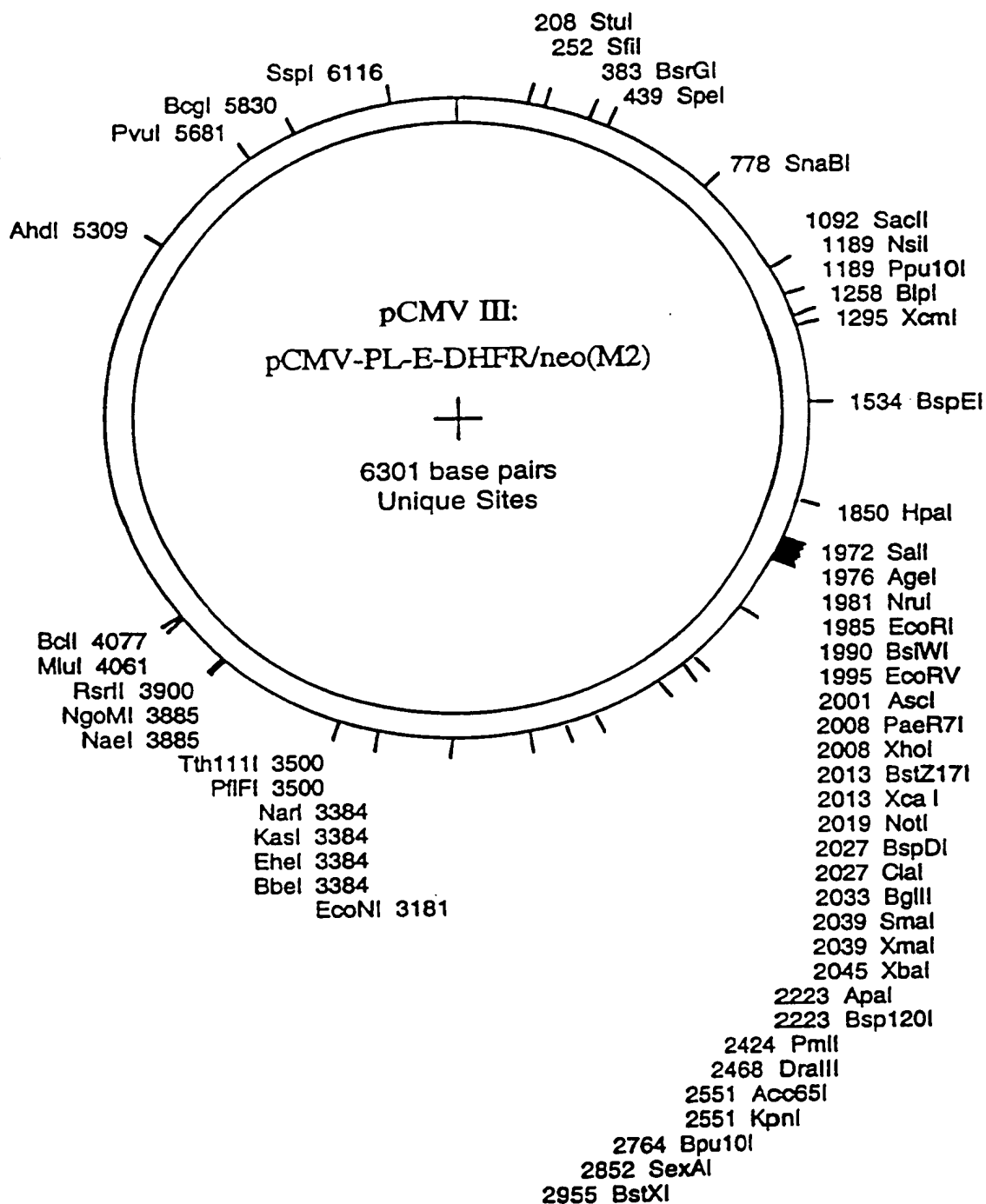


FIG. 13B

24 / 131

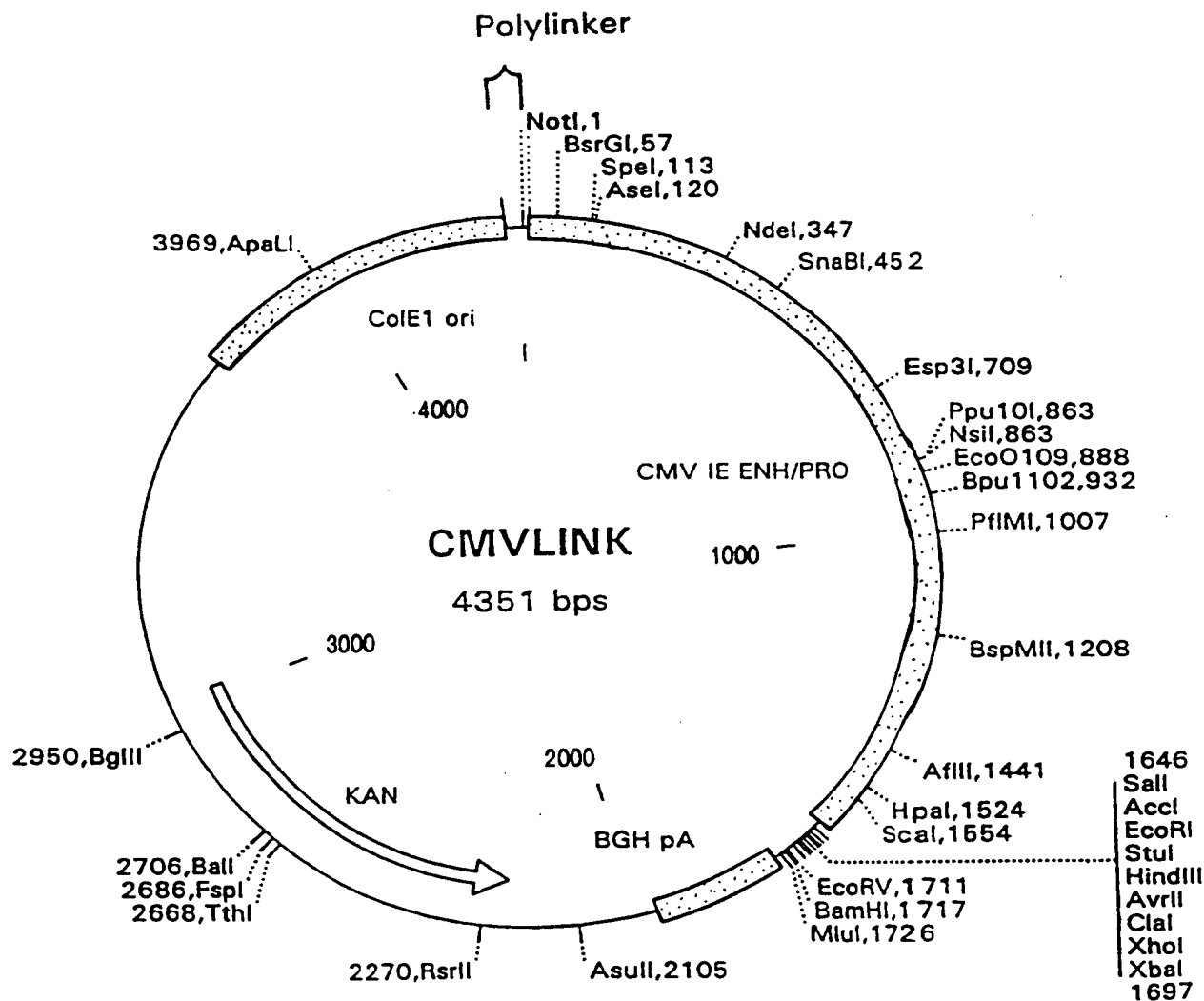


FIG. 14

25 / 131

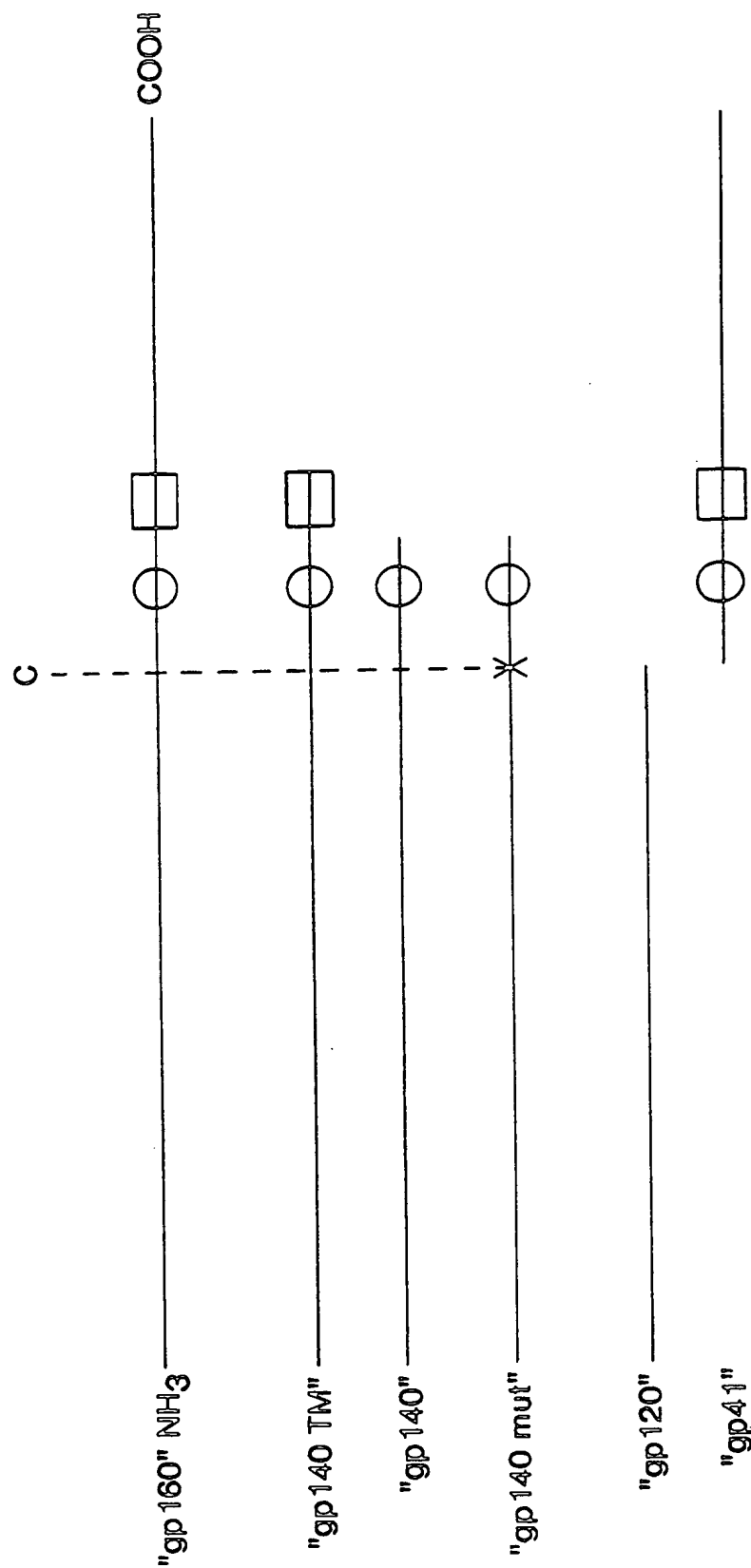


FIG. 15

26 / 131

gp120wtSF162

GTAGAAAAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGAAAGAAGCAACCACCTCTATTTT
GTGCATCAGATGCTAAAGCCTATGACACAGAGGTACATAATGTCTGGGCCACACATGCCCTGTGTACCCAC
AGACCTAACCCACAAGAAATAGTATTGGAAAAATGTACAGAAAAATTTAACATGTGGAAAAATAACATG
GTAGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAGTCTAAAGCCATGTGTAAAGTTAAACCC
CACTCTGTGTACTCTACATTCACATAATTGGAAGAAATGCTACTAATACCAAGAGTAGTAATTGGAAAGA
GATGGACAGAGGAGAAAAATAAAAAATTGCTCTTTCAAGGTCACCAAGCATTAAGAAATAAGATGCAGAAA
GAATATGCACCTTTTTTATAAACTTGATGTAGTACCATAAGATAATGATAATACAGCTATAAAATTGATAA
ATTGTAACACCTCAGTCATTACACAGGCCGTGTCCAAAGGTATCCTTTGAACCAATTCCCATACATTATTG
TGCCCCGGCTGTTTTGCGATTCTAAAGTGTAAATGATAAGAAAGTTCAATGGATCAGGACCATGTACAAAT
GTCAGCACAGTACAATGTACACATGGAAATTAGGCCAGTAGTGTCAACTCAATTGCTGTTAAATGGCAGTC
TAGCAGAAAGAAGGGTAGTAATTAGATCTGAAAAATTTACAGACAAATGCTAAAACTATAATAGTACAGCT
GAAGGAATCTGTAGAAAAATTAAATTGTACAGACCTAACATAATAAGAAAAAGTATAACTATAGGACCG
GGGAGAGCATTTTATGCAACAGGAGACATAATAGGAGATATAAGACAAGCACATTGTTAACATTAGTGGAG
AAAAATGGAATAACACTTTTAAACAGATAGTTACAAAAATTACAAAGCACAAATTTGGGAAATAAAACAATAGT
CTTTAAGCAATCCCTCAGGAGGGGACCCAGAAATTGTAATGCACAGTTTAAATTGTGGAGGGGAATTTTC
TACTGTAAATTCACACACAGCTTTTAAATAGTACTTGGAAATAATACTATAGGGCCAAATAACACTAATGGAA
CTATCACACTCCCATGCAGAAATAAAACAAATTATAAAACAGGTGGCAGGAAGTAGGAAAAGCAATGTATGC
CCCTCCCATCAGAGGACAAATTAGATGCTCATCAAAATAATTACAGGACTGCTATTAAACAAGAGATGGTGGT
AAAGAGATCAGTAACACCCCGAGATCTTCAGACCTGGAGGTGGAGATATGAGGGACAATTGGAGAAAGTG
AATTATATAAAATATAAAGTAGTAAAAATTGAGCCATTAGGAGTAGCACCCACCAAGGCAAGAGAAAGAGT
GGTGCAGAGAGAAAAAAGA

FIG. 16
(SEQ ID NO:30)

27 / 131

gp140wtSF162

GTAGAAAAATTGTGGGTACAGTCTATTATGGGGTACCTGTGTGGAAAGAAAGCAACCACCCTCTATTTT
GTGCATCAGATGCTAAAGCCTATGACACAGAGGTACATAAATGTCTGGGCCACACATGCCTGTGTACCCAC
AGACCCCTAACCCACAAGAAATAGTATTGGAAAAATGTGACAGAAAAATTTTAAACATGTGGAAAAATAACATG
GTAGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAAGTCTAAAGCCCATGTGTAAAGTTAAACCC
CACTCTGTGTTACTCTACATTGCACCTAATTGGAAGAAATGCTACTAATACCAAGAGTAGTAATTGGAAAAA
GATGGACAGAGAGAGAAATAAAAAATTTGCTCTTTCAAGGTCACCAAGCATAAAGAAATAAGATGCAGAAA
GAATATGCACCTTTTATAAACTTGATGTAGTACCAATAGATAATAGATAATACAAGCTATAAAATTGATAA
ATTGTAAACACCTCAGTCATTACACAGGCCGTGCCAAAGGTATCCTTTGAAACCAATTTCCCATACATTATTG
TGCCCGGCTGGTTTGGGATTTCAAGTGTAAAGTATAAGAAAGTTCAATGGATCAGGACCATGTACAAAT
GTCAGCACAGTACAAATGTACACATGGAATTAGGCCAGTAGTGTCAACTCAATTGCTGTTAAATGGCAGTC
TAGCAGAAAGAGGGTAGTAATTAGATCTGAAAAATTTACAGACAAATGCTAAAACTATAATAGTACAGCT
GAAGGAATCTGTAGAAATTAAATTGTACAAGACCTAAACAATAACAAGAAAAAGTATAACTATAGGACCG
GGGAGAGCATTTTATGCAACAGGAGACATAATAGGAGATATAAGACAAGCACATTTGTAACATTAGTGGAG
AAAAATGGAATAACACTTTAAAAACAGATAGTTACAAAAATTACAAGCACAAATTTGGGAATAAAAACAATAGT
CTTTAAGCAATCCTCAGGAGGGGCCAGAAATTGTAATGCACAGTTTAAATTGTGGAGGGGAATTTTTC
TACTGTAAATTCAAACACAGCTTTTAAATAGTACTTGGAAATAATACTATAGGGCCAAATAACACTAATGGAA
CTATCACACTCCCATGCAGAAATAAAACAAATTATAAACAGGTGGCAGGAAGTAGGAAAAGCAATGTATGC
CCCTCCCATCAGAGGACAAATTAGATGCTCATCAAAATAATTACAGGACTGCTATTAAACAGAGATGGTGGT
AAAGAGATCAGTAACACCCAGAGATCTTCAGACCTGGAGGTGGAGATATGAGGACAAATTGGAGAAGTG
AATTATATAAATAATAAGTAGTAAAAATTGAGCCATTAGGAGTAGCACCCACCAAGGCAAGAGAAAGAGT
GGTGCAGAGAGAAAAAAGAGCAGTGACGCTAGGAGCTATGTTCTTGGGTTCTTGGGAGCAGCAGGAAGC
ACTATGGGCGCACGGTCACTGACGCTGACGGTACAGGCCAGACAAATTATTGTCTGGTATAGTGCAACAGC
AGAACAAATTTGCTGAGAGCTATTGAGGCGCAACAGCATCTGTTGCAACTCACAGTCTGGGCGATCAAGCA
GCTCCAGGCAAGAGTCTGGCTGTGGAAAGATACCTAAAGGATCAACAGCTCCTAGGGATTGGGGTTGC
TCTGGAAAACTCATTTGCACCACTGCTGTGCTTGGAAATGCTAGTTGGAGTAATAAATCTCTGGATCAGA
TTTGGAAATAACATGACCTGGAATGGAGTGGGAGAGAGAAATTGACAAATTACAAAACTTAATATACACCTT
AATTGAAGAATCGCAGAACCAACAAGAAAAAGAAATGAACAAGAAATTATTAGAAATTGGATAAGTGGGCAAGT
TTGTGGAAATTGGTTTGACATATCAAAATGGCTGTGGTATATA

FIG. 17

(SEQ ID NO:31)

28 / 131

gp160wtSF162

GTAGAAAAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGAAGCAACCACCACTCTATTTT
GTGCATCAGATGCTAAAGCCTATGACACAGAGGTACATAATGTCTGGGCCACACATGCCTGTGTACCCAC
AGACCCTAACCACAAGAAATAGTATTGGAAAATGTGACAGAAAATTTTAACATGTGGAAAAATAACATG
GTAGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAGTCTAAAGCCATGTGTAAAGTTAACCC
CACTCTGTGTTACTCTACATTGCACTAATTTGAAGAATGCTACTAATACCAAGAGTAGTAATTGGAAAGA
GATGGACAGAGGAGAAATAAAAAATTGCTCTTTCAAGGTCACCACAAGCATAAGAAATAAGATGCAGAAA
GAATATGCACTTTTTTATAAACTTGATGTAGTACCAATAGATAATGATAATACAAGCTATAAAATTGATAA
ATTGTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTGAACCAATTCCCATACATTATTG
TGCCCCGGCTGGTTTTTGCATTCTAAAGTGTAAATGATAAGAAGTTCAATGGATCAGGACCATGTACAAAT
GTCAGCAGTAGTACAATGTACACATGGAATTAGGCCAGTAGTGTCAACTCAATTGCTGTTAAATGGCAGTC
TAGCAGAAGAAGGGGTAGTAATTAGATCTGAAAATTTACAGACAATGCTAAACTATAATAGTACAGCT
GAAGGAATCTGTAGAAATTAATTGTACAAGACCTAACAATAATACAAGAAAAAGTATAACTATAGGACCG
GGGAGAGCATTTTATGCAACAGGAGACATAATAGGAGATATAAGACAAGCACATTGTAACATTAGTGGAG
AAAAATGGAATAACACTTTAAACAGATAGTTACAAAATTACAAGCACAAATTTGGGAATAAAACAATAGT
CTTTAAGCAATCCTCAGGAGGGGACCCAGAAATTGTAATGCACAGTTTTTAATTGTGGAGGGGAATTTTTT
TACTGTAATTCACACAGCTTTTTAATAGTACTTGAATAATACTATAGGGCCAAATAACACTAATGGAA
CTATCACACTCCCATGCAGAATAAAACAAATTATAAACAGGTGGCAGGAAGTAGGAAAAGCAATGTATGC
CCCTCCCATCAGAGGACAAATTAGATGCTCATCAATATTACAGGACTGCTATTAACAAGAGATGGTGGT
AAAGAGATCAGTAACACCACCGAGATCTTCAGACCTGGAGGTGGAGATATGAGGGACAATTGGAGAAGTG
AATTATATAAATATAAAGTAGTAAAAATTGAGCCATTAGGAGTAGCACCCACCAAGGCAAAGAGAAGAGT
GGTGCAGAGAGAAAAAAGAGCAGTGACGCTAGGAGCTATGTTCTTGGGTTCTTGGGAGCAGCAGGAAGC
ACTATGGGCGCACGGTCACTGACGCTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCAACAGC
AGAACAATTTGCTGAGAGCTATTGAGGCGCAACAGCATCTGTTGCACTCACAGTCTGGGGCATCAAGCA
GCTCCAGGCAAGAGTCCTGGCTGTGGAAGATACCTAAAGGATCAACAGCTCCTAGGGATTTGGGGTTGC
TCTGGAATACTCATTTGCACCACTGCTGTGCCTTGAATGCTAGTTGGAGTAATAAATCTCTGGATCAGA
TTTGGAATAACATGACCTGGATGGAGTGGGAGAGAGAAATTGACAATTACACAACTTAATATACACCTT
AATTGAAGAATCGCAGAACCAACAAGAAAAGAATGAACAAGAATTATTAGAATTGGATAAGTGGGCAAGT
TTGTGGAATTGGTTTGACATATCAAAATGGCTGTGGTATATAAAAAATATTCATAATGATAGTAGGAGTT
TAGTAGGTTTAAGGATAGTTTTTACTGTGCTTCTATAGTGAATAGAGTTAGGCAGGGATACTCACCATT
ATCATTTTCAGACCCGCTTCCCAGCCCCAAGGGGACCCGACAGGCCCGAAGGAATCGAAGAAGAAGGTGGA
GAGAGAGACAGAGACAGATCCAGTCCATTAGTGCATGGATTATTAGCACTCATCTGGGACGATCTACGGA
GCCTGTGCCTCTTCAGCTACCACCGCTTGAGAGACTTAATCTTGATTGCAGCGAGGATTGTGGAACCTCT
GGGACGCAGGGGGTGGGAAGCCCTCAAGTATTGGGGGAATCTCCTGCAGTATTGGATTTCAGGAACCTAAAG
AATAGTGCTGTAGTTTGTGTTGATGCCATAGCTATAGCAGTAGCTGAGGGGACAGATAGGATTATAGAAG
TAGCACAAAGAATTGGTAGAGCTTTTCTCCACATACCTAGAAGAATAAGACAGGGCTTTGAAAGGGCTTT
GCTATAA

FIG. 18
(SEQ ID NO:32)

29 / 131

gp120.modSF162

gaattcgccaccatggatgcaatgaagagagggtctgctgtgtgctgtgtgtgagcagtc
 ttcgtttcgccagcgccgtggagaagctgtgggtgacctgtactacggcgtgcccggtgtggaag
 gagccaccaccaccctgttctgcgccagcgacgccaaggcctacgacaccgaggtgcacaacgtg
 tggccaccaccacgcctgctgcccaccgaccccaacccccaggagatcgtgctggagaacgtgacc
 gagaacttcaacatgtggaagaacaacatggtggagcagatgcacgaggacatcatcagcctgtgg
 gaccagagcctgaagcctgctgaagctgacccccctgtgctgacctgcactgcaccaacctg
 aagaacgccaccaacacagagcagcaactggaaggagatggaccggcgagatcaagaactgc
 agcttcaaggtgaccaccagcatccgcaacaagatgcagaaggagtacgcccctgttctacaagctg
 gacgtggtgccatcgacaacgacaacaccagctacaagctgatcaactgcaacaccagcgtgatc
 accagggcctgcccagggtgagcttcgagccccatccccactccactactgcgcccccgccgttc
 gccatcctgaagtgaacgacacaagaagtccaacggcagcgccccctgcaccaacgtgagcaccgtg
 cagtgacccacggcatccgccccgtggtgagcaccacagctgctgctgaacggcagcctggccgag
 gagggcgtggtgatccgcagcgagaaacttcaccgacaacgccaagaccatcatcgtgcagctgaag
 gagagcgtggagatcaactgcacccgcccccaacaacacccgcaagagcatcaccatcgcccc
 ggccgccccttctacgccaccggcgacatcatcgcgacatccgccaggccccactgcaacatcagc
 ggcgagaagtggaaacaacacccctgaagcagatcgtgaccaagctgcaggccccagttcggcaacaag
 accatcgtgtcaagcagagcagcgcgccgaccccgagatcgtgatgcacagcttcaactgcggc
 ggcgagttcttctactgcaacagcaccacagctgttcaacagcacctggaaacaacacatcgcccc
 aacaacacacggcacccatcacccctgccctgccgcatcaagcagatcatcaaccgtggcaggag
 gtgggcaaggccatgtacgccccccccatccgcgccagatccgctgcagcagcaacatcacccggc
 ctgctgctgacccgcgacggcggaaggagatcagcaacacaccacagatcttccgccccggcggc
 ggcgacatgcgcgacaactggcgacgagctgtacaagtacaaggtggtgaagatcgagccccctg
 ggcgtggccccccaccaaggccaagcgccgctggtgcagcgcgagaagcgctaactcgag

FIG. 19**(SEQ ID NO:33)**

30 / 131

gp120.modSF162.delV2

gaattcgccaccatggatgcaatgaagagagggctctgctgtgtgctgctgtgtggagcagtc
ttcgtttcgcccagcgcgtggagaagctgtgggtgacctgtactacggcgtgcccggtggaag
gagccaccaccacctgttctgcccagcgacgccaaaggcctacgacaccgaggtgcacaacgtg
tggccaccacgcctgctgcccacgaccccccaacccccaggagatcgtgctggagaaactgacc
gagaacttcaacatgtggaagaacaacatggtggagcagatgcacgaggacatcatcagcctgtgg
gaccagacctgaagccctgctgaagctgacccccctgtgctgacctgcaactgcaccaacctg
aagaacgcccacaacacgaagagcagcaactggaaggagatggaccgcgcgagatcaagaactgc
agcttcaagggtggcgccggaagctgatcaactgcaacaccagcgtgatcaccaggcctgcccc
aaggtagcttcgagcccatccccatccactactgcccccccgccgcttcgccatcctgaagtgc
aacgacaagaagtcaacggcagcgccccctgcaccaacgtgagcacctgcagtgcaccacggc
atccgccccgtgtgagcaccacagctgctgctgaacggcagcctggccgaggagggcgtgtgac
cgagcgagaacttcaccgacaacgccaagaccatcatcgtgcagctgaaggagagcgtggagatc
aactgcaccgcccccaacaacacccgcaagagatcaccatcgcccccgccgcttctac
gccaccggcgacatcatcggcgacatccgccaggccccactgcaacatcagcggcgagaagtggaa
aacacctgaagcagatcgtgaccaagctgcaggccccagtcggcaacaagaccatcgtgtcaag
cagagcagcggcgaccccgagatcgtgatgcacagcttcaactcgggcgagttcttctac
tgcaacagcacccagctgttcaacagcacctggaacaacaccatcgcccccaacaacacacggc
accatcacctgccctgccgcatcaagcagatcatcaaccgctggcaggaggtgggcaaggccatg
tacgcccccccatccgcgccagatccgctgcagcagcaacatcacccgctgctgctgacccgc
gacggcggaaggagatcagcaacacacccagatcttcgccccggcgcgacatgcgcgac
aactggcgagcagctgtacaagtacaagggtggtgaagatcgagccccctggcgctggccccacc
aaggccaagcgcgcgtggtgcagcgagagaagcgtcaactcgag

FIG. 20

(SEQ ID NO:34)

[illegible]

FIG. 21
(SEQ ID NO:35)

32 / 131

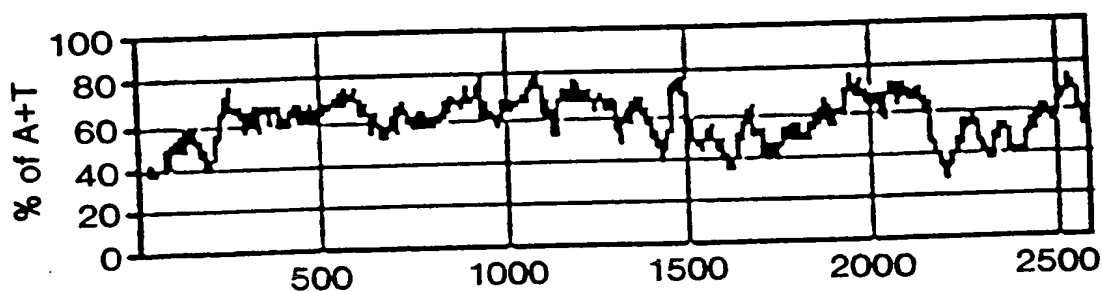


FIG. 22A

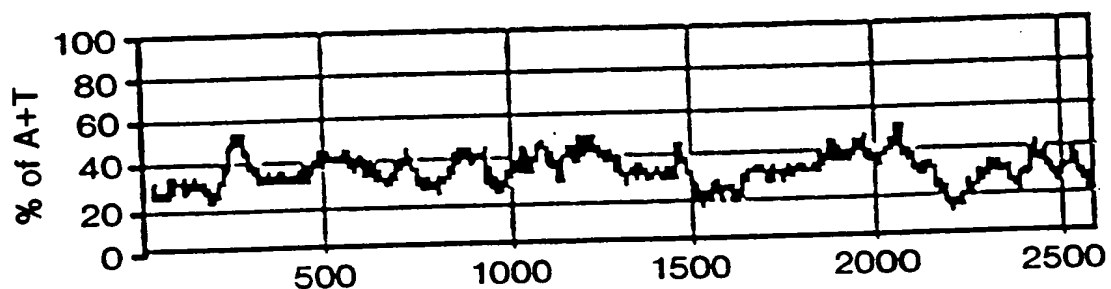


FIG. 22B

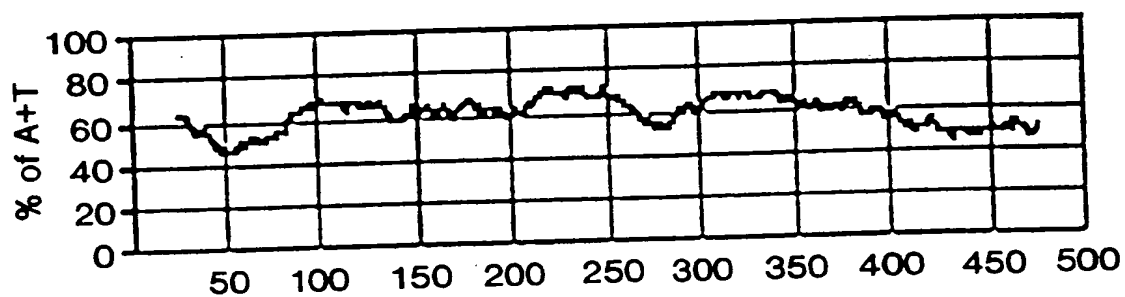


FIG. 22C

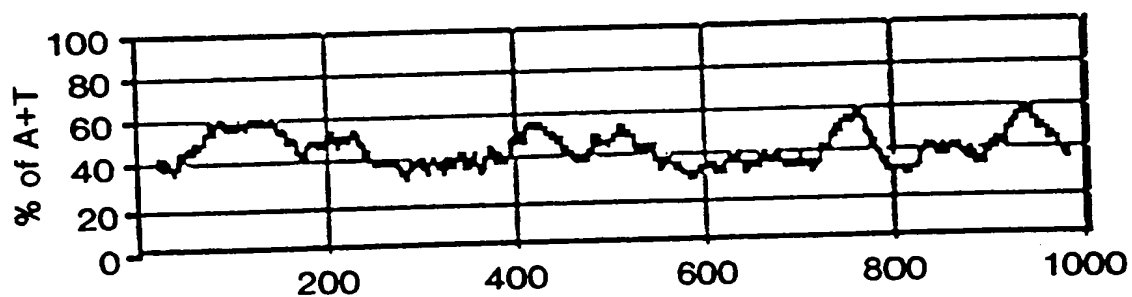


FIG. 22D

SUBSTITUTE SHEET (RULE 26)

33 / 131

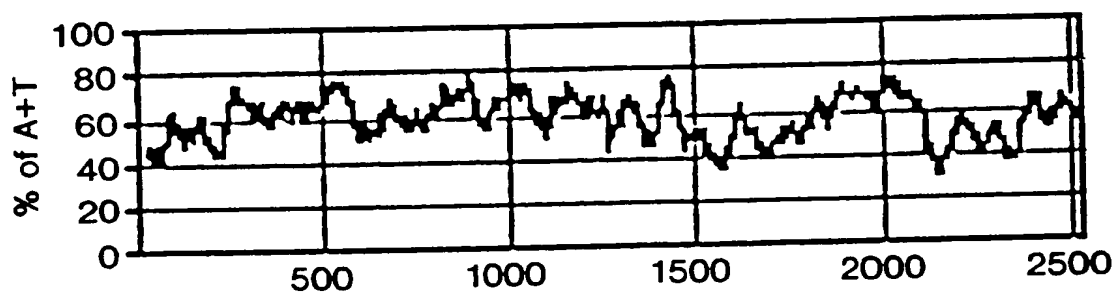


FIG. 22E

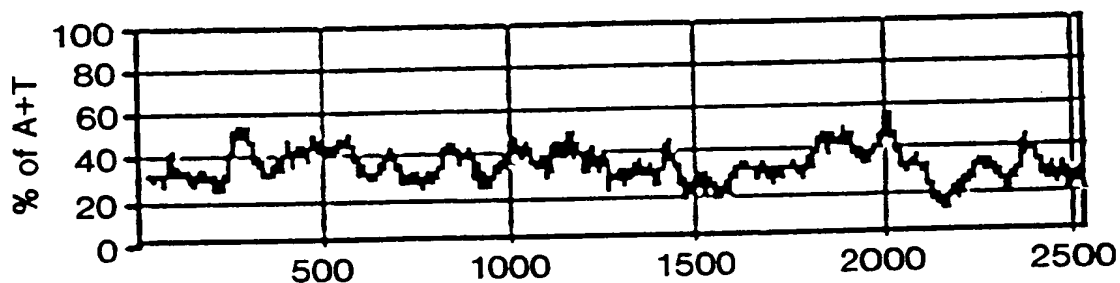


FIG. 22F

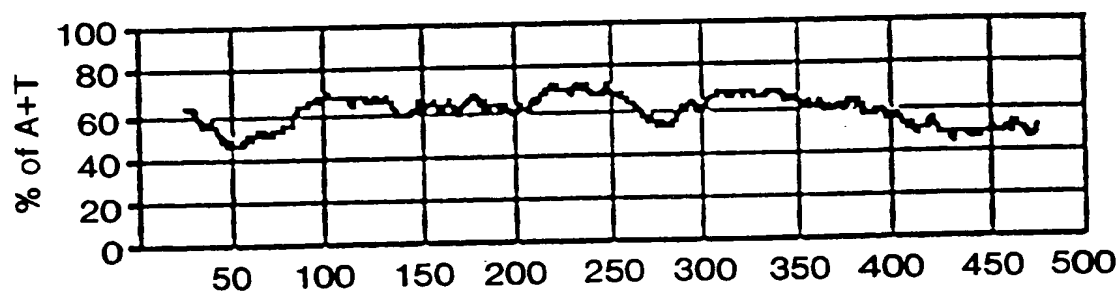


FIG. 22G

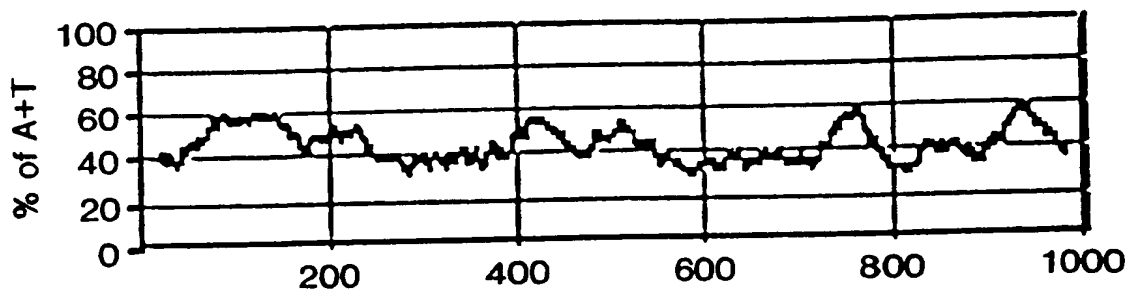


FIG. 22H

SUBSTITUTE SHEET (RULE 26)

gp140.modSF162

gaattcgccaccatggatgcaatgaagagaggggtctctgctgtgtgctgctgctgtgtgtggagcagtc
ttcgtttcgcccagcgccgtggagaagctgtgggtgaccgtgtactacggcggtgcccgtgtggaag
gagggccaccaccacctgttctgcgccagcgacgccaaggcctacgacaccgaggtgcacaacgtg
tggggccaccacgcctgctgcccaccgaccccaacccccaggagatcgtgctggagaacgtgacc
gagaacttcaacatgtggaagaacaacatgggtggagcagatgcacgaggacatcatcagcctgtgg
gaccagagcctgaagccctgctggaagctgacccccctgtgctgacccctgcactgcaccaacctg
aagaacgccaccaacaccaagagcagcaactggaaggagatggaccgcggcgagatcaagaactgc
agcttcaagggtgaccaccagcatccgcaacaagatgcagaaggagtagcgcctgttctacaagctg
gacgtggtgcccacgacaacgacaacaccagctacaagctgatcaactgcaacaccagcgtgatc
accagggcctgccccaaagggtgagcttcgagcccatcccatccactactgcgcccccgccggcttc
gccatcctgaagtgcacgacaagaagtccaacggcgagcgccccctgcaccaacgtgagcaccgtg
cagtgacccacggcatccgccccgtggtgagcaccagctgctgctgaacggcgagcctggccgag
gagggcgtggtgatccgagcgagaacttcaccgacaacgccaagaccatcatcgtgcagctgaag
gagagcgtggagatcaactgcaccgcccccaacaacacccgcaagagcatcaccatcgggcccc
ggcgcgccttctacgccaccggcgacatcatcgggcgacatccgcccaggcccactgcaacatcagc
ggcgagaagtggaaacaacacctgaagcagatcgtgaccaagctgcaggcccagttcgggaacaag
accatcgtgttcaagcagagcagcgggcgaccccgagatcgtgatgcacagcttcaactgcggc
ggcgagttcttctactgcaacagcaccagctgttcaacagcacctggaacaacaccatcgggcccc
aacaacaccaacggcaccatcaccctgcccctgcccgcacatcaagcagatcatcaaccgctggcaggag
gtgggcaaggccatgtacgcccccccccatccgcgggccagatccgctgcagcagcaacatcaccggc
ctgctgctgacccgcgacggcggaaggagatcagcaacaccaccgagatcttccgccccggcggc
ggcgacatgcgcgacaactggcgagcgagctgtacaagtacaagggtggtgaagatcgagccccctg
ggcgtggccccccaccaaggccaagcgccgcgtggtgcagcgcgagaagcgcgccgtgacccctgggc
gccatgttcctgggcttcctgggcgcccgcggcagcaccatggggcgcccgcagcctgacccctgacc
gtgcaggccccgcagctgctgagcggcatcgtgcagcagcagacaacctgctgcgcgccatcgag
gcccagcagcacctgctgcagctgacccgtgtggggcatcaagcagctgcaggcccgcgtgctggcc
gtggagcgctacctgaaggaccagcagctgctgggcatctggggctgcagcggcaagctgatctgc
accaccgcccgtgcccctggaacgccagctggagcaacaagagcctggaccagatctggaacaacatg
acctggatggagtgaggagcgagatcgacaactacaccaacctgatctacaccctgatcgaggag
agccagaaccagcaggagaagaacgagcaggagctgctggagctggacaagtggggccagcctgtgg
aactgggttcgacatcagcaagtggctgtggtacatctaactcgag

FIG. 23

(SEQ ID NO:36)

35/131

gp140.modSF162.delV2

gaattcgccaccatggatgcaatgaagagagggctctgctgtgtgctgctgctgtgtggagcagtc
ttcgtttcgcccagcgccgtggagaagctgtgggtgaccgtgtactacggcgtgcccgtgtggaag
gaggccaccaccacctgttctgcgccagcgacgccaaggcctacgacaccgaggtgcacaacgtg
tgggccacccacgcctgctgcccaccgaccccaacccccaggagatcgtgctggagaacgtgacc
gagaacttcaacatgtggaagaacaacatgggtggagcagatgcacgaggacatcatcagcctgtgg
gaccagagcctgaagccctgctggaagctgacccccctgtgctgacccctgcactgcaccaacctg
aagaacgccaccaacaccaagagcagcaactggaaggagatggaccgcccgcgagatcaagaactgc
agcttcaaggtgggcgcccggcaagctgatcaactgcaacaccagcgtgatcaccagggcctgcccc
aaggtgagcttcgagcccatcccatccactactgcgcccccgccggcttcgccatcctgaagtgc
aacgacaagaagtccaacggcagcggccctgcaccaacgtgagcaccgtgcagtgcaccacggc
atccgccccctgggtgagcaccagctgctgctgaacggcagcctggccgaggagggcggtgatc
cgcagcgagaacttcaccgacaacgccaaagaccatcatcgtgcagctgaaggagagcgtggagatc
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gccaccggcgacatcatcggcgacatccgccaggcccaactgcaacatcagcggcgagaagtggaa
aacaccctgaagcagatcgtgaccaagctgcaggcccaagtccggcaacaagaccatcgtgttcaag
cagagcagcggcgggcgacccccgagatcgtgatgcacagcttcaactgcggcgggcgagttcttctac
tgcaacagcaccagctgttcaacagcacctggaacaacaccatcgggcccaacaacaccaacggc
accatcaccctgcccctgcccgcacatcaagcagatcatcaaccgctggcaggaggtgggcaaggccatg
taagcccccccccatccgcggccagatccgctgcagcagcaacatcaccggcctgctgctgacccgc
gacggcggcaaggagatcagcaacaccaccgagatcttccgccccggcgggcgacatgcgcgac
aactggcgagcgagctgtacaagtacaaggtgggtgaagatcgagccctggggcgtggccccacc
aaggccaagcggcgctgggtgcagcgcgagaagcgcgcctgacccctgggcgcatgttctgggc
ttcctgggcgcccgcggcagcaccatgggcgcccgcagcctgacccctgacccgtgcaggcccgccag
ctgctgagcggcatcgtgcagcagcagaacaacctgctgcgcgccatcgaggccagcagcacctg
ctgcagctgacccgtgtggggcatcaagcagctgcaggcccgctgctggcgtggagcgctacctg
aaggaccagcagctgctgggcatctggggctgcagcggcaagctgatctgcaccaccgcccgtgccc
tggaaacgccagctggagcaacaagagcctggaccagatctggaacaacatgacctggatggagtgg
gagcgcgagatcgacaactacaccaacctgatctacaccctgatcgaggagagccagaaccagcag
gagaagaacgagcaggagctgctggagctggacaagtgggcccagcctctggaactgggttcgacatc
agcaagtggctgtggtacatctaactcgag

FIG. 24
(SEQ ID NO:37)

36 / 131

gp140.modSF162.delV1V2

gaattcgccaccatggatgcaatgaagagagggctctgctgtgtgctgctgctgtgtggagcagtc
ttcgtttcgcccagcgccgtggagaagctgtgggtgaccgtgtactacggcgtgcccgtgtggaag
gaggccaccaccacctgttctgcgccagcgacgccaaggcctacgacaccgaggtgcacaacgtg
tgggccaccacgcctgctgcccaccgaccccaacccccaggagatcgtgctggagaacgtgacc
gagaacttcaacatgtggaagaacaacatgggtggagcagatgcacgaggacatcatcagcctgtgg
gaccagagcctgaagccctgctggaagctgacccccctgtgctggtggcgccggcaactgccagacc
agcgtgatcaccacaggcctgccccaaagggtgagcttcgagcccatccccatccactactgcgcccc
gccggcttcgccatcctgaagtgaacgacaagaagtccaacggcagcggccccctgcaccaacgtg
agcaccgtgcagtgacccacggcatccgccccgtgggtgagcaccacagctgctgctgaacggcagc
ctggccgagggagggcggtgatccgcagcgagaacttcaccgacaacgccaagaccatcatcgtg
cagctgaaggagagcgtggagatcaactgcaccgcgcccccaacaacaacacccgcaagagcatcacc
atcgcccccgccgcgccttctacgccaccggcgacatcatcggcgacatccgcccaggccactgc
aacatcagcggcgagaagtgaacaacaccctgaagcagatcgtgaccaagctgcaggcccagttc
ggcaacaagaccatcgtgttcaagcagagcagcggcgccgacccccgagatcgtgatgcacagcttc
aactgcggcgggcgagttcttctactgcaacagcaccacagctgttcaacagcacctggaacaacacc
atcgcccccaacaacaccaacggcaccatcaccctgccttgcgcgatcaagcagatcatcaaccgc
tggcaggaggtgggcaaggccatgtacgccccccccatccgcggccagatccgctgcagcagcaac
atcaccggcctgctgctgacccgcgacggcgggcaaggagatcagcaacaccaccgagatcttccgc
cccgcgggcgggcgacatgcgcgacaactggcgagcagcagctgtacaagta caagggtgggtgaagatc
gagccccctggcggtggcccccaaggccaagcgccgcgtgggtgcagcgcgagaagcgcgccgtg
accctgggcgcccattgttcttgggcttcttgggcgcccgcggcagcaccatgggcgcccgcagcctg
accctgaccgtgcaggccccgcagctgctgagcggcatcgtgcagcagcagaacaacctgctgcgc
gccatcgaggcccagcagcaccctgctgcagctgaccgtgtggggcatcaagcagctgcaggcccgc
gtgctggccgtggagcgctacctgaaggaccagcagctgctgggcatctggggctgcagcggcaag
ctgatctgcaccaccgcgctgccctggaacgccagctggagcaacaagagcctggaccagatctgg
aacaacatgacctggatggagtgggagcgcgagatcgacaactacaccaacctgatctacacctg
atcgaggagagccagaaccagcaggagaagaacgagcaggagctgctggagctggacaagtgggcc
agcctgtggaactgggtcgacatcagcaagtggctgtggtacatctaactcgag

FIG. 25

(SEQ ID NO:38)

37 / 131

gp140.mut.modSF162

gaattcgccaccatggatgcaatgaagagagggctctgctgtgtgctgctgctgtgtgtggagcagtc
ttcgtttcgcccagcgccgtggagaagctgtgggtgaccgtgtactacggcgtgcccgtgtggaag
gaggccaccaccacctgttctgcgccagcgacgccaaggcctacgacaccgaggtgcacaacgtg
tgggcccaccacgcctgctgcccaccgaccccaacccccaggagatcgtgctggagaacgtgacc
gagaacttcaacatgtggaagaacaacatggtggagcagatgcacgaggacatcatcagcctgtgg
gaccagagcctgaagccctgctggaagctgacccccctgtgctgacccctgcactgcaccaacctg
aagaacgccaccaacaccaagagcagcaactggaaggagatggaccgcggcgagatcaagaactgc
agcttcaagggtgaccaccagcatccgcaacaagatgcagaaggagtacgccctgttctacaagctg
gacgtggtgcccacgacaacaccagctacaagctgatcaactgcaacaccagcgtgatc
accagggcctgccccaaagggtgagcttcgagcccatcccatccactactgcgccccgcgggcttc
gccatcctgaagtgaacgacaagaagtcaacggcagcggccccctgcaccaacgtgagcaccgtg
cagtgcaccacggcatccgccccgtggtgagcaccacagctgctgctgaacggcagcctggccgag
gagggcgtggtgatccgcagcgagaacttcaccgacaacgcccaagaccatcatcgtgcagctgaag
gagagcgtggagatcaactgcaccgcgccccacaacaacaccgcgaagagcatcaccatcgggccc
ggcgcgccttctacgccaccggcgacatcatcggcgacatccgcccaggcccactgcaacatcagc
ggcgagaagtggaaacaacacctgaagcagatcgtgaccaagctgcaggcccagttcggaacaag
accatcgtgttcaagcagagcagcggcgggcgaccccgagatcgtgatgcacagcttcaactgcggc
ggcgagtcttctactgcaacagcaccagctgttcaacagcacctggaacaacaccatcgggccc
aacaacaccaacggcaccatcaccttgccctgcccgcacatcaagcagatcatcaaccgctggcaggag
gtggggcaaggccatgtacgcccccccatccgcgccagatccgctgcagcagcaacatcacgggc
ctgctgctgaccgcgcagggcggaaggagatcagcaacaccaccgagatcttcgccccggcggc
ggcgacatgcgcgacaactggcgcgagcagctgtacaagtacaagggtggtgaagatcgagccctg
ggcgtggccccccaccaaggccaagcgccgcgtggtgcagcgcgagaagagcgccgtgacctgggc
gccatgttcctgggcttcctggggcgccgcggcagcaccatgggcgcccgcagcctgacctgacc
gtgcaggccccgcagctgctgagcgccatcgtgcagcagcagaacaacctgctgcgcgccatcgag
gcccagcagcacctgctgcagctgaccgtgtgggscatcaagcagctgcaggccccgctgctggcc
gtggagcgtacctgaaggaccagcagctgctgggcatctggggctgcagcggcaagctgatctgc
accaccgcgtgcccctggaacgccagctggagcaacaagagcctggaccagatctggaacaacatg
acctggatggagtgggagcgcgagatcgacaactacaccaacctgatctacacctgatcgaggag
agccagaaccagcaggagaagaacgagcaggagctgctggagctggacaagtgggcccagcctgtgg
aactggttcgacatcagcaagtggctgtggtacatctaactcgag

FIG. 26

(SEQ ID NO:39)

38 / 131

gp140.mut.modSF162.delV2

gaattcgccaccatggatgcaatgaagagagggctctgctgtgtgctgctgctgtgtggagcagtc
ttcgtttcgcccagcgccgtggagaagctgtgggtgaccgtgtactacggcggtgcccgtgtggaag
gaggccaccaccacctgttctgcgccagcgacgccaaggcctacgacaccgaggtgcacaacgtg
tgggccaccacgcctgctgcccaccgaccccaacccccaggagatcgtgctggagaacgtgacc
gagaacttcaacatgtggaagaacaacatggtggagcagatgcacgaggacatcatcagcctgtgg
gaccagagcctgaagccctgctggaagctgacccccctgtgctgaccctgcactgcaccaacctg
aagaacgcccaccaacaccaagagcagcaactggaaggagatggaccgcggcgagatcaagaactgc
agcttcaaggtgggcgccggcaagctgatcaactgcaacaccagcgtgatcacccaggcctgcccc
aaggtgagcttcgagcccatccccatccactactgcgcccccgccggcttcgccatcctgaagtgc
aacgacaagaagttcaacggcagcgccccctgcaccaacgtgagcaccgtgcagtgcaccacggc
atccgccccgtggtgagcaccagctgctgctgaacggcagcctggccgaggagggcggtgatc
cgcagcgagaacttcaccgacaacgccaagaccatcatcgtgcagctgaaggagagcgtggagatc
aactgcacccgcccccaacaacaacacccgcaagagcatcaccatcgcccccggccgcgccttctac
gccaccggcgacatcatcgggcgacatccgccaggccccactgcaacatcagcggcgagaagtggaa
aacaccctgaagcagatcgtgaccaagctgcaggcccagttcggcaacaagaccatcgtgttcaag
cagagcagcggcgggcgaccccgagatcgtgatgcacagcttcaactgcggcgggcgagtcttctac
tgcaacagcaccagctgttcaacagcacctggaacaacaccatcgcccccacaacaacaccaacggc
accatcaccttgccctgcccgcacatcaagcagatcatcaaccgctggcaggagggtgggcaaggccatg
tacgcccccccccatccgcgggccagatccgctgcagcagcaacatcacccggcctgctgctgacccgc
gacggcgggcaaggagatcagcaacaccaccgagatcttcgccccggcgggcggcgacatgcgcgac
aactggcgcgagcagctgtacaagtacaaggtgggtgaagatcgagccccctgggcgtggccccacc
aaggccaagcgccgcgtggtgcagcgcgagaagagcgccgtgaccctgggcgcccattgttcttgggc
ttcctggggcgccgcccggcagcaccatggggcgcccgagcctgaccctgaccgtgcaggccccgcccag
ctgctgagcggcatcgtgcagcagcagaacaacctgctgcgcgccatcgaggcccagcagcaccctg
ctgcagctgaccgtgtggggcatcaagcagctgcaggcccgcgtgctggcgtggagcgctacctg
aaggaccagcagctgctggggcatctggggctgcagcggcaagctgatctgcaccaccgcccgtgcc
tggaacgcccagctggagcaacaagagcctggaccagatctggaacaacatgacctggatggagtgg
gagcgcgagatcgacaactacaccaacctgatctacacctgatcgaggagagccagaaccagcag
gagaagaacgagcaggagctgctggagctggacaagtgggcccagocctgtggaactggttcgacatc
agcaagtggctgtggtacatctaactcgag

FIG. 27
(SEQ ID NO:40)

39 / 131

gp140.mut.modSF162.delV1V2

gaattcgccaccatggatgcaatgaagagagggctctgctgtgtgctgctgctgtgtgtggagcagtc
ttcgtttcgcccagcgccgtggagaagctgtgggtgaccgtgtactacggcgtgcccgtgtggaag
gagggcaccaccaccctgttctgcgccagcgacgccaaggcctacgacaccgaggtgcacaacgtg
tggggcaccacgcctgctgcccaccgaccccaacccccaggagatcgtgctggagaacgtgacc
gagaacttcaacatgtggaagaacaacatgggtggagcagatgcacgaggacatcatcagcctgtgg
gaccagagcctgaagccctgctggaagctgacccccctgtgctggtggcgccggcaactgccagacc
agcgtgatcaccagggcctgccccaaaggtgagcttcgagcccatcccatccactactgcgcccc
gccggcttcgccatcctgaagtgcacgacaagaagtccaacggcagcgccccctgcaccaacgtg
agcaccgtgcagtgacccacggcatccgccccgtgggtgagcaccagctgctgctgaacggcagc
ctggccgaggagggcggtgatccgcagcgagaacttcaccgacaacgccaagaccatcatcgtg
cagctgaaggagagcgtggagatcaactgcacccgcccccaacaacaacccgcaagagcatcacc
atcgcccccgccgcgccttctacgccaccggcgacatcatcggcgacatccgcccaggccactgc
aacatcagcgccgagaagtgaacaacaccctgaagcagatcgtgaccaagctgcaggccagttc
ggcaacaagaccatcgtgttcaagcagagcagcgggcgacccccgagatcgtgatgcacagcttc
aactgcggcgccgagttcttctactgcaacagcaccagctgttcaacagcacctggaacaacacc
atcgcccccaacaacaccaacggcaccatcacctgcccgtccgcacatcaagcagatcatcaaccgc
tggcaggaggtgggcaaggccatgtacgccccccccatccgcccgcagatccgctgcagcagcaac
atcacccggcctgctgctgacccgcgacggcgccgaaggagatcagcaacaccaccgagatcttccgc
cccggcgggcgccgacatgcgcgacaactggcgccagcgagctgtacaagtacaaggtgggtgaagatc
gagccccctggcgctggcccccaacaaggccaagcgccgcgtgggtgcagcgcgagaagagcgccgtg
accctggcgccatgttcttgggcttccctggggcgccgcccgcagcaccatgggcgcccgcagcctg
accctgaccgtgcaggccccgcagctgctgagcgccatcgtgcagcagcagaacaacctgctgcgc
gccatcgaggcccagcagcacctgctgcagctgaccgtgtggggcatcaagcagctgcaggcccg
gtgctggccgtggagcgctacctgaaggaccagcagctgctggggcatctggggctgcagcggaag
ctgatctgcaccaccgcccgtgccctggaacgccagctggagcaacaagagcctggaccagatctgg
aacaacatgacctggatggagtgggagcgcgagatcgacaactacaccaacctgatctacacctg
atcgaggagagccagaaccagcaggagaagaacgagcaggagctgctggagctggacaagtgggccc
agcctgtggaactgggttcgacatcagcaagtggctgtggtacatctaactcgag

FIG. 28

(SEQ ID NO:41)

40 / 131

gp140.mut7.modSF162

gaattcgccaccatggatgcaatgaagagagggctctgctgtgtgctgctgctgtgtggagcagtc
ttcggtttcgcccagcgccgtggagaagctgtgggtgaccgtgtactacggcgtgcccgtgtggaag
gaggccaccaccaccctgttctgcgccagcgacgccaaggcctacgacaccgaggtgcacaacgtg
tgggcccaccacgcctgctgcccaccgaccccaacccccaggagatcgtgctggagaacgtgacc
gagaacttcaacatgtggaagaacaacatgggtggagcagatgcacgaggacatcatcagcctgtgg
gaccagagcctgaagccctgctggaagctgacccccctgtgctgaccctgcactgcaccaacctg
aagaacgccaccaacaccaagagcagcaactggaaggagatggaccgcccgcagatcaagaactgc
agcttcaaggtgaccaccagcatccgcaacaagatgcagaaggagtagccctgttctacaagctg
gacgtggtgcccacgacaacaccagctacaagctgatcaactgcaacaccagcgtgatc
accaggcctgccccaaaggtgagcttcgagcccatcccatccactactgcgcccccgccggcttc
gccatcctgaagtgcacgacaagaagtccaacggcagcggccccctgcaccaacgtgagcacctgtg
cagtgcacccacggcatccgccccgtggtgagcacccagctgctgctgaacggcagcctggccgag
gagggcgtggtgatccgcagcgagaacttcaccgacaacgcccaagaccatcatcgtgcagctgaag
gagagcgtggagatcaactgcaccgcccccaacaacaacaccgcgaagagcatcaccatcgcccc
ggccgcgcccttctacgccaccggcgacatcatcggcgacatccgccaggcccactgcaacatcagc
ggcgagaagtggaaacaacacctgaagcagatcgtgaccaagctgcaggcccagttcggaacaag
accatcgtgttcaagcagagcagcggcgccgagaccccgagatcgtgatgcacagcttcaactgcggc
ggcgagtcttctactgcaacagcacccagctgttcaacagcacctggaacaacaccatcgcccc
aacaacaccaacggcaccatcacctgccctgccgcatcaagcagatcatcaaccgctggcaggag
gtgggcaaggccatgtacgcccccccatccgcggccagatccgctgcagcagcaacatcacggc
ctgctgctgaccgcgacggcggaaggagatcagcaacaccaccgagatcttccgccccggcggc
ggcgacatgcgcgacaactggcgagcagctgtacaagtacaaggtggtgaagatcgagccctg
ggcgtggccccccaccaaggccatcagcagcgtggtgcagagcgagaagagcgcctgaccctgggc
gccatgttccctgggcttccctgggcgcccggcagcaccatgggcgcccgcagcctgaccctgacc
gtgcaggccccgcagctgctgagcggcatcgtgcagcagcagaacaacctgctgcgcgccatcgag
gcccagcagcacctgctgcagctgaccgtgtggggcatcaagcagctgcaggcccgcgtgctggcc
gtggagcgctacctgaaggaccagcagctgctgggcctctggggctgcagcggcaagctgatctgc
accaccgcccgtgccctggaacgccagctggagcaacaagagcctggaccagatctggaacaacatg
acctggatggagtgggagcgcgagatcgacaactacaccaacctgatctacacctgatcgaggag
agccagaaccagcaggagaagaacgagcaggagctgctggagctggacaagtgggcccagcctgtgg
aactggttcgacatcagcaagtggctgtggtacatctaactcgag

FIG. 29

(SEQ ID NO:42)

41 / 131

gp140.mut7.modSF162.delV2

gaattcgccaccatggatgcaatgaagagagggctctgctgtgtgctgctgctgtgtggagcagtc
ttcggtttcgcccagcgccgtggagaagctgtgggtgaccgtgtactacggcgtgcccgtgtggaag
gaggccaccaccaccctgttctgcgccagcgacgccaaggcctacgacaccgaggtgcacaacgtg
tgggccaccacgcctgctgcccaccgaccccaacccccaggagatcgtgctggagaacgtgacc
gagaacttcaacatgtggaagaacaacatgggtggagcagatgcacgaggacatcatcagcctgtgg
gaccagagcctgaagccctgctggaagctgacccccctgtgctgaccctgcactgcaccaacctg
aagaacgccaccaacaccaagagcagcaactggaaggagatggaccgcggcgagatcaagaactgc
agcttcaaggtgggcgccggcaagctgatcaactgcaacaccagcgtgatcaccaggcctgcccc
aaggtgagcttcgagcccattcccatccactactgcgcccccgccggttcgccatcctgaagtgc
aacgacaagaagtcaacggcagcgccccctgcaccaacgtgagcaccgtgcagtgcaccacggc
atccgccccgtggtgagcaccagctgctgctgaacggcagcctggccgaggagggcggtgatc
cgcagcgagaacttcaccgacaacgccaagaccatcatcgtgcagctgaaggagagcgtggagatc
aactgcacccgcccccaacaacacaccgcaagagcatcaccatcgggccccggccgcgccttctac
gccaccggcgacatcatcggcgacatccgccaggccactgcaacatcagcggcgagaagtggaaac
aacaccctgaagcagatcgtgaccaagctgcaggcccagttcggaacaagaccatcgtgttcaag
cagagcagcggcgggcgaccccgagatcgtgatgcacagcttcaactgcggcgggcgagttcttctac
tgcaacagcaccagctgttcaacagcacctggaacaacaccatcgggcccccaacaacaccaacggc
accatcaccctgcccctgcccgcacatcaagcagatcatcaaccgctggcaggaggtgggcaaggccatg
tacgccccccccatccgcgccagatccgctgcagcagcaacatcaccggcctgctgctgaccgcg
gacggcgggcaaggagatcagcaacaccaccgagatcttccgccccggcgggcgacatgcgcgac
aactggcgcgagcgagctgtacaagtacaaggtggtgaagatcgagcccctgggctggccccacc
aaggccatcagcagcgtggtgcagagcgagaagagcgccgtgaccctgggcgccatgttccctgggc
ttccctgggcgccgcccggcagcaccatgggcgccccgagcctgaccctgaccgtgcaggccccgcca
ctgctgagcggcatcgtgcagcagcagaacaacctgctgcgcgccatcgaggcccagcagcacctg
ctgcagctgaccgtgtggggcatcaagcagctgcaggccccgctgctggcctggagcgctacctg
aaggaccagcagctgctgggcatctggggctgcagcggcaagctgatctgcaccaccgcccgtgcc
tggaacgccagctggagcaacaagagcctggaccagatctggaacaacatgacctggatggagtgg
gagcgcgagatcgacaactacaccaacctgatctacacctgatcgaggagagccagaaccagcag
gagaagaacgagcaggagctgctggagctggacaagtgggcccagcctgtggaactggttcgacatc
agcaagtggctgtggtacatctaactcgag

FIG. 30
(SEQ ID NO:43)

42 / 131

gp140.mut7.modSF162.delV1V2

gaattcgccaccatggatgcaatgaagagagggctctgctgtgtgctgctgctgtgtggagcagtc
ttcggtttcgcccagcgccgtggagaagctgtgggtgaccgtgtactacggcgtgcccgtgtggaag
gagggcaccaccaccctgttctgcgccagcgacgccaaggcctacgacaccgaggtgcacaacgtg
tgggccacccacgcctgcggtgcccaccgaccccaacccccaggagatcgtgctggagaacgtgacc
gagaacttcaacatgtggaagaacaacatgggtggagcagatgcacgaggacatcatcagcctgtgg
gaccagagcctgaagccctgcggtgaagctgacccccctgtgctggggcgccggcaactgccagacc
agcgtgatcaccagggcctgccccaaaggtgagcttcgagcccatccccatccactactgcgcccc
gccggcttcgccatcctgaagtgcaacgacaagaagttaacggcagcggccccctgcaccaacgtg
agcaccgtgcagtgcaaccacggcatccgccccgtggtgagcaccacagctgctgctgaacggcagc
ctggccgaggagggcggtggtgatccgcagcgagaacttcaccgacaacgccaagaccatcatcgtg
cagctgaaggagagcgtggagatcaactgcacccgccccaaacaacaccccgcaagagcatcacc
atcgggccccggccgcgcttctacgccaccggcgacatcatcgggcagatccgcccaggccccactgc
aacatcagcggcgagaagtggaaacaacaccctgaagcagatcgtgaccaagctgcaggccccagttc
ggcaacaagaccatcgtgttcaagcagagcagcggcgggcgacccccgagatcgtgatgcacagcttc
aactgcggcgggcgagttcttctactgcaacagcaccacagctgttcaacagcacctggaacaacacc
atcgggccccaacaacaccaacggcaccatcacctgccccgcccgcacatcaagcagatcatcaaccgc
tggcaggaggtgggcaaggccatgtacgccccccccatccgoggccagatccgctgcagcagcaac
atcacccggcctgctgctgacccgcgacggcggaaggagatcagcaaacaccaccgagatcttccgc
ccggcgggcgggcgacatgcgcgacaactggcgcgagcagctgtacaagtacaaggtgggtgaagatc
gagccccctggcggtggcccccaaggccatcagcagcgtggtgcagagcgagaagagcgccgtg
accctggggcgccatgttcttgggcttcttggggcgccggccggcagcaccatggggcgcccgagcctg
accctgaccgtgcaggccccgcccagctgctgagcggcatcgtgcagcagcagaacaacctgctgcgc
gccatcgaggcccagcagcacctgctgcagctgaccgtgtggggcatcaagcagctgcaggccccgc
gtgctggccgtggagcgctacctgaaggaccagcagctgctggggcatctggggctgcagcggcaag
ctgatctgcaccaccgcccgtgccctggaacgccagctggagcaacaagagcctggaccagatctgg
aacaacatgacctggatggagtgggagcgcgagatcgacaactacaccaacctgatctacacctg
atcgaggagagccagaaccagcaggagaagaacgagcaggagctgctggagctggacaagtgggcc
agcctgtggaactgggttcgacatcagcaagtggctgtggtacatctaactcgag

FIG. 31

(SEQ ID NO:44)

43 / 131

gp140.mut8.modSF162

gaattcgccaccatggatgcaatgaagagagggctctgctgtgtgctgctgctgtgtggagcagtc
ttcggttcgcccagcgccgtggagaagctgtgggtgaccgtgtactacggcgtgcccgtgtggaag
gaggccaccaccaccctgttctgcgccagcgacgccaaggcctacgacaccgaggtgcacaacgtg
tggggccaccacgcctgctgcccaccgaccccaacccccaggagatcgtgctggagaacgtgacc
gagaacttcaacatgtggaagaacaacatgggtggagcagatgcacgaggacatcatcagcctgtgg
gaccagagcctgaagccctgctggaagctgacccccctgtgctgacccctgcactgcaccaacctg
aagaacgccaccaacaccaagagcagcaactggaaggagatggaccgcggcgagatcaagaactgc
agcttcaaggtgaccaccagcatccgcaacaagatgcagaaggagtacgcccctgttctacaagctg
gacgtggtgcccacgacaacaccagctacaagctgatcaactgcaacaccagcgtgatc
acccaggcctgcccccaaggtgagcttcgagcccatcccatccactactgcgcccccgccggcttc
gccatcctgaagtgaacgacaagaagttcaacggcagcggccccctgcaccaacgtgagcaccgtg
cagtgcacccacggcatccgccccgtggtgagcaccagctgctgctgaacggcagcctggccgag
gagggcgtggtgatccgcagcgagaacttcaccgacaacgcccaagaccatcatcgtgcagctgaag
gagagcgtggagatcaactgcacccgcccccaacaacaacacccgcaagagcatcaccatcggcccc
ggccgcgccttctacgccaccggcgacatcatcggcgacatccgccaggcccactgcaacatcagc
ggcgagaagtggaaacaacacctgaagcagatcgtgaccaagctgcaggcccagttcggcaacaag
accatcgtgttcaagcagagcagcggcgggcgaccccgagatcgtgatgcacagcttcaactgcggc
ggcgagtcttctactgcaacagcaccagctgttcaacagcacctggaacaacaccatcggcccc
aacaacaccaacggcaccatcacctgcccctgccgcacatcaagcagatcatcaaccgctggcaggag
gtgggcaaggccatgtacgccccccccatccgcggccagatccgctgcagcagcaacatcacgggc
ctgctgctgaccgcgacggcggaaggagatcagcaacaccaccgagatcttccgccccggcggc
ggcgacatgcgcgacaactggcgagcagctgtacaagtacaaggtggtgaagatcgagcccctg
ggcgtggccccaccatcgccatcagcagcgtggtgcagagcgagaagagcgccgtgacctgggc
gccatgttcttgggttcttggggcgccgcccgcagcaccatggggcgcccgagcctgacctgacc
gtgcaggccccggcagctgctgagcggcatcgtgcagcagcagaacaacctgctgcgcgccatcgag
gcccagcagcacctgctgcagctgaccgtgtggggcatcaagcagctgcaggcccgcgtgctggcc
gtggagcgtacctgaaggaccagcagctgctggggcatctggggctgcagcggcaagctgatctgc
accaccgcccgtgccctggaacgccagctggagcaacaagagcctggaccagatctggaacaacatg
acctggatggagtgggagcgcgagatcgacaactacaccaacctgatctacacctgatcgaggag
agccagaaccagcaggagaagaacgagcaggagctgctggagctggacaagtgggcccagcctgtgg
aactggttcgacatcagcaagtggctgtggtacatctaactcgag

FIG. 32
(SEQ ID NO:45)

44 / 131

gp140.mut8.modSF162.delV2

gaattcgccaccatggatgcaatgaagagagggctctgctgtgtgctgctgctgtgtggagcagtc
ttcgtttcgcccagcgccgtggagaagctgtgggtgaccgtgtactacggcgtgcccgtgtggaag
gaggccaccaccacctgttctgcgccagcgacgccaaggcctacgacaccgaggtgcacaacgtg
tgggccaccacgcctgctgcccaccgaccccaacccccaggagatcgtgctggagaacgtgacc
gagaacttcaacatgtggaagaacaacatggtggagcagatgcacgaggacatcatcagcctgtgg
gaccagagcctgaagccctgctggaagctgacccccctgtgctgaccctgcactgcaccaacctg
aagaacgccaccaacaccaagagcagcaactggaaggagatggaccgcggcgagatcaagaactgc
agcttcaaggtgggcgccggcaagctgatcaactgcaacaccagcgtgatcaccaggcctgcccc
aaggtgagcttcgagcccatccccatccactactgcgcccccgccggcttcgccatcctgaagtgc
aacgacaagaagttcaacggcagcgccccctgcaccaacgtgagcaccgtgcagtgcaccacggc
atccgccccgtggtgagcaccagctgctgctgaacggcagcctggccgaggaggggcgtggtgatc
cgcagcgagaacttcaccgacaacgccaagaccatcatcgtgcagctgaaggagagcgtggagatc
aactgcaccgcgcccaacaacaacaccccgcaagagcatcaccatcggccccggccgcgccttctac
gccaccggcgacatcatcggcgacatccgcccaggcccactgcaacatcagcggcgagaagtggaaac
aacaccctgaagcagatcgtgaccaagctgcaggcccagttcggcaacaagaccatcgtgttcaag
cagagcagcggcgggcgacccccgagatcgtgatgcacagcttcaactgcggcgggcgagttcttctac
tgcaacagcaccagctgttcaacagcacctggaacaacaccatcggcccccaacaacaccaacggc
accatcacccctgcccctgcccgcacatcaagcagatcatcaaccgctggcaggaggtggggaaggccatg
tacgcccccccccatccgcgggccagatccgctgcagcagcaacatcacccggcctgctgctgaccgcg
gacggcgggcaaggagatcagcaacaccaccgagatcttccgccccggcgggcgggcgacatgcgcgac
aactggcgcgagcagctgtacaagtacaaggtggtgaagatcgagccccctgggctggccccccacc
atcgccatcagcagcgtggtgcagagcgagaagagcgccgtgacccctgggcgccatgttcctgggc
ttcctgggcgccgcccggcagcaccatgggcgccccgcagcctgacccctgaccgtgcaggccccgcccag
ctgctgagcggcatcgtgcagcagcagaacaacctgctgcgcgccatcgaggcccagcagcacctg
ctgcagctgaccgtgtggggcatcaagcagctgcaggcccgcgtgctggccgtggagcgtacctg
aaggaccagcagctgctgggcatctggggctgcagcggcaagctgatctgcaccaccgcccgtgccc
tggaaacgccagctggagcaacaagagcctggaccagatctggaacaacatgacctggatggagtgg
gagcgcgagatcgacaactacaccaacctgatctacaccctgatcgaggagagccagaaccagcag
gagaagaacgagcaggagctgctggagctggacaagtgggcccagcctgtggaactggttcgacatc
agcaagtggctgtggtacatctaactcgag

FIG. 33

(SEQ ID NO:46)

45/ 131

gp140.mut8.modSF162.delV1V2

gaattcgccaccatggatgcaatgaagagagggctctgctgtgtgctgctgctgtgtggagcagtc
ttcgtttcgcccagcgccgtggagaagctgtgggtgaccgtgtactacggcgtgcccgtgtggaag
gaggccaccaccacctgttctgcgccagcgacgccaaggcctacgacaccgaggtgcacaacgtg
tgggccaccacgcctgcgtgcccaccgaccccaacccccaggagatcgtgctggagaacgtgacc
gagaacttcaacatgtggaagaacaacatggtggagcagatgcacgaggacatcatcagcctgtgg
gaccagagcctgaagccctgcgtgaagctgacccccctgtgcgtgggcgcggcaactgccagacc
agcgtgatcaccagggcctgccccaaaggtgagcttcgagcccatcccatccactactgcgcccc
ggcggcttcgccatcctgaagtgcacgacaagaagttcaacggcagcggccccctgcaccaacgtg
agcaccgtgcagtgacccacggcatccgccccgtggtgagcaccagctgctgctgaacggcagc
ctggccgaggaggcggtggtgatccgcagcgagaacttcaccgacaacgccaagaccatcatcgtg
cagctgaaggagagcgtggagatcaactgcaccgcgcccaacaacaacaccgcgaagagcatcacc
atcgcccccgccgcgcttctacgccaccggcgacatcatcggcgacatccgcccaggcccactgc
aacatcagcggcgagaagtggaaacaacaccctgaagcagatcgtgaccaagctgcaggcccagttc
ggcaacaagaccatcgtgttcaagcagagcagcggcgggcgaccccgagatcgtgatgcacagcttc
aactgcggcgggcgagtcttcttactgcaacagcaccagctgttcaacagcacctggaacaacacc
atcgcccccaacaacaccaacggcaccatcacccctgcccctgcgcgatcaagcagatcatcaaccgc
tggcaggaggtgggcaaggccatgtacgcccccccccatccgcggccagatccgctgcagcagcaac
atcacccggcctgctgctgacccgcgacggcgggcaaggagatcagcaacaccaccgagatcttccgc
cccgccggcgggcgacatgcgcgacaactggcgcgagcagctgtacaagtacaagggtggtgaagatc
gagccccctgggcgtggccccccaccatcgccatcagcagcgtggtgcagagcgagaagagcgccgtg
accctgggcgcccgtgttcttgggcttcttgggcgcccggcgagcaccatgggcgcccgcagcctg
accctgaccgtgcaggccccgcagctgctgagcggcatcgtgcagcagcagaacaacctgctgcgc
gccatcgaggcccagcagcacctgctgcagctgaccgtgtggggcatcaagcagctgcaggcccgc
gtgctggccgtggagcgctacctgaaggaccagcagctgctggggcatctggggctgcagcggcaag
ctgatctgcaccaccgcccgtgcccctggaacgccagctggagcaacaagagcctggaccagatctgg
aacaacatgacctggatggagtgggagcgcgagatcgacaactacaccaacctgatctacacctg
atcgaggagagccagaaccagcaggagaagaacgagcaggagctgctggagctggacaagtgggcc
agcctgtggaactggttcgacatcagcaagtggctgtggtacatctaactcgag

FIG. 34

(SEQ ID NO:47)

46 / 131

gp160.modSF162

gaattcgccaccatggatgcaatgaagagagggctctgctgtgtgctgctgctgtgtggagcagtc
ttcgtttcgcccagcgccgtggagaagctgtgggtgaccgtgtactacggcgtgcccgtgtggaag
gaggccaccaccacctgttctgcgccagcgacgccaaggcctacgacaccgaggtgcacaacgtg
tggggcaccacgcctgctgcccaccgaccccaacccccaggagatcgtgctggagaacgtgacc
gagaacttcaacatgtggaagaacaacatggtggagcagatgcacgaggacatcatcagcctgtgg
gaccagagcctgaagccctgctggaagctgacccccctgtgctgaccctgcactgcaccaacctg
aagaacgccaccaacaccaagagcagcaactggaaggagatggaccgcggcgagatcaagaactgc
agcttcaaggtgaccaccagcatccgcaacaagatgcagaaggagtacgccctgttctacaagctg
gacgtggtgcccacgacaacgacaacaccagctacaagctgatcaactgcaacaccagcgtgatc
accaggcctgcccgaaggtgagcttcgagcccatcccatccactactgcgcccccgccggcttc
gccatcctgaagtgcaacgacaagaagttcaacggcagcgggccctgcaccaacgtgagcaccgtg
cagtgcacccacggcatccgccccgtggtgagcaccagctgctgctgaacggcagcctggccgag
gagggcgtggtgatccgcagcgagaacttcaccgacaacgccaagaccatcatcgtgcagctgaag
gagagcgtggagatcaactgcaaccgcccccaacaacaacaccgcaagagcatcaccatcgggccc
ggccgcgccttctacgccaccggcgacatcatcggcgacatccgccaggccactgcaacatcagc
ggcgagaagtggaacaacaccctgaagcagatcgtgaccaagctgcaggcccagttcggcaacaag
accatcgtgttcaagcagagcagcgggcgacccccgagatcgtgatgcacagcttcaactgcggc
ggcgagttcttctactgcaacagcaccagctgttcaacagcacctggaacaacaccatcgggccc
aacaacaccaacggcaccatcacctgccctgcgcgcatcaagcagatcatcaaccgctggcaggag
gtgggcaaggccatgtacgccccccccatccgcggccagatccgctgcagcagcaacatcacggc
ctgctgctgacccgcgacggcggaaggagatcagcaacaccaccgagatcttccgccccggcggc
ggcgacatgcgcgacaactggcgcgagcagctgtacaagtacaaggtggtgaagatcgagccctg
ggcgtggccccaccaaggccaagcgccgcgtggtgcagcgcgagaagcgcgccgtgacctgggc
gccatgttccctgggcttccctgggcgcgcggcgagcaccatgggcgcccgcagcctgacctgacc
gtgcaggcccgcagctgctgagcggcatcgtgcagcagcagaacaacctgctgcgcgccatcgag
gcccagcagcacctgctgcagctgacctgtggggcatcaagcagctgcaggcccgcgtgctggcc
gtggagcgctacctgaaggaccagcagctgctgggcatctggggctgcagcggcaagctgatctgc
accaccgccgtgccctggaacgcccagctggagcaacaagagcctggaccagatctggaacaacatg
acctggatggagtgggagcgcgagatcgacaactacaccaacctgatctacacctgatcgaggag
agccagaaccagcaggagaagaacgagcaggagctgctggagctggacaagtggggcagcctgtgg
aactggttcgacatcagcaagtggctgtggtacatcaagatcttcatcatgatcgtgggcggcctg
gtgggcctgcgcacgtgttaccgtgctgagcatcgtgaaccgctgcgcagggctacagcccc
ctgagcttcagacccgcttccccgccccccgcggcccccgaccgccccgagggcatcgaggaggag
ggcgggcagcgcgaccgcgaccgcagcagccccctggtgcacggcctgctggccctgatctgggac
gacctgcgcagcctgtgctgttcagctaccaccgctgcgcgacctgatcctgatcgccgccccg
atcgtggagctgctgggcccgcgcggctgggaggccctgaagtactggggcaacctgctgcagtac
tggatccaggagctgaagaacagcgccgtgagcctgttcgacgccatcgccatcgccgtggccgag
ggcaccgaccgcatcatcgaggtggccagcgcatcgccgcgccttccctgcacatccccgcgcg
atccgccagggttcgagcgcgccctgctgtaactcgag

FIG. 35

(SEQ ID NO:48)

47 / 131

gp160.modSF162.delV2

gaattcgccaccatggatgcaatgaagagaggggctctgctgtgtgctgctgctgtgtggagcagtc
ttcggtttcgcccagcgccgtggagaagctgtgggtgaccgtgtactacggcgtgcccgtgtggaag
gaggccaccaccacctgttctgcgccagcgacgccaaggcctacgacaccgaggtgcacaacgtg
tgggccacccacgcctgctgcccaccgaccccaacccccaggagatcgtgctggagaacgtgacc
gagaacttcaacatgtggaagaacaacatgggtggagcagatgcacgaggacatcatcagcctgtgg
gaccagagcctgaagccctgctggaagctgacccccctgtgctgacccctgcactgcaccaacctg
aagaacgccaccaacaccaagagcagcaactggaaggagatggaccgaggcgagatcaagaactgc
agcttcaaggtggggcgccggcaagctgatcaactgcaacaccagcgtgatcaccaggcctgcccc
aaggtgagcttcgagcccatccccatccactactgcgcccccgccggcttcgccatcctgaagtgc
aacgacaagaagttcaacggcagcgcccccctgcaccaacgtgagcaccgtgcagtgcaccacggc
atccgccccgtggtgagcaccagctgctgctgaacggcagcctggccgaggaggcggtggtgatc
cgcagcgagaacttcaccgacaacgccaagaccatcatcgtgcagctgaaggagagcgtggagatc
aactgcaccgcgcccaacaacaacacccgcaagagcatcaccatcgccccggccgcgcccttctac
gccaccggcgacatcatcgggcagatccgcccaggcccactgcaacatcagcggcgagaagtggaaac
aacaccctgaagcagatcgtgaccaagctgcaggcccagttcggcaacaagaccatcgtgttcaag
cagagcagcggcgggcgaccccgagatcgtgatgcacagcttcaactgcggcgggcgagttcttctac
tgcaacagcaccagctgttcaacagcacctggaacaacaccatcgggcccaacaacaccaacggc
accatcaccttgccctgcccgcacatcaagcagatcatcaaccgctggcaggaggtgggcaaggccatg
tacgcccccccccatccgcgggccagatccgctgcagcagcaacatcacccggcctgctgctgacccgc
gacggcggaaggagatcagcaacaccaccgagatcttccgccccggcgggcgggcgacatgcgcgac
aactggcgcgagcgtgtacaagtacaaggtggtgaagatcgagccctggggcggtggccccccacc
aaggccaagcgccgctggtgcagcgcgagaagcgcgccgtgacccctggggcgccatgttccctgggc
ttcctggggcgccgcccggcagcaccatggggcgcccgagcctgacccctgaccgtgcaggccccgcccag
ctgctgagcggcatcgtgcagcagcagaacaacctgctgcgcgccatcgaggcccgagcagcacctg
ctgcagctgaccgtgtggggcatcaagcagctgcaggccccgctgctggcgctggagcgctacctg
aaggaccagcagctgctgggcatctggggctgcagcggaagctgatctgcaccaccgcccgtgccc
tggaacgccagctggagcaacaagagcctggaccagatctggaacaacatgacctggatggagtgg
gagcgcgagatcgacaactacaccaacctgatctacaccctgatcgaggagagccagaaccagcag
gagaagaacgagcaggagctgctggagctggacaagtgggcccagcctgtggaactggttcgacatc
agcaagtggctgtggtacatcaagatcttcatcatgatcgtggggcgccctgggtgggcctgcgcac
gtgttcaccgtgctgagcatcgtgaaccgctgcccagggttacagccccctgagcttccagacc
cgcttccccgcccccccgcgccccgaccgccccgagggcatcgaggaggaggggcgggcgagcgcgac
cgcgaccgcagcagccccctggtgcacggcctgctggccctgatctgggacgacctgcgcagcctg
tgccctgttcagctaccaccgctgcccgcacctgatccctgatcgccgccccgcatcgtggagctgctg
ggccgcccggctgggaggccctgaagtactggggcaacctgctgcagtactggatccaggagctg
aagaacagcggcgtgagcctgttcgacgccatcgccatcgccgtggccgagggccaccgaccgcac
atcgaggtggcccagcgcacatcgggcgcgcccttctgacatcccccgccgcatccgcccagggttc
gagcgcgccttgcgtgtaactcgag

FIG. 36

(SEQ ID NO:49)

48 / 131

gp160.modSF162.delV1V2

gaattcgccaccatggatgcaatgaagagaggggctctgctgtgtgctgctgctgtgtggagcagtc
ttcgtttcgcccagcgccgtggagaagctgtgggtgaccgtgtactacggcgtgcccgtgtggaag
gaggccaccaccacctgttctgcgccagcgacgccaaggcctacgacaccgaggtgcacaacgtg
tggggccaccacgcctgctgcccaccgacccaacccccaggagatcgtgctggagaacgtgacc
gagaacttcaacatgtggaagaacaacatgggtggagcagatgcacgaggacatcatcagcctgtgg
gaccagagcctgaagccctgctggaagctgacccccctgtgctggtgggcgcgggcaactgccagacc
agcgtgatcaccaggcctgcccccaagggtgagcttcgagcccatccccatccactactgcgcccc
gccggcttcgccatcctgaagtgcacgacaagaagttcaacggcagcggccccctgcaccaacgtg
agcaccgtgcagtgacccacggcatccgccccgtggtgagcaccagctgctgctgaacgggcagc
ctggccgaggagggcggtggtgatccgcagcgagaacttcaccgacaacgcgaagaccatcatcgtg
cagctgaaggagagcgtggagatcaactgcacccgcccccaacaacacaccgcaagagcatcacc
atcgcccccgccgcgcccttctacgccaccggcgacatcatcgccgacatccgccaggccccactgc
aacatcagcggcgagaagtggaaacaacaccctgaagcagatcgtgaccaagctgcaggcccagttc
ggcaacaagaccatcgtgttcaagcagagcagcggcgccgagaccccgagatcgtgatgcacagcttc
aactgcggcgggcgagttcttctactgcaacagcaccagctgttcaacagcacctggaacaacacc
atcgcccccaacaacaccaacggcaccatcaccctgccctgccgcatcaagcagatcatcaaccgc
tggcaggaggtgggcaaggccatgtacgcccccccccatccgcggccagatccgctgcagcagcaac
atcacccggcctgctgctgacccgcgacggcgggcaaggagatcagcaacacaccgagatcttccgc
cccggcgggcgacatgcgcgacaactggcgcgagcagctgtacaagta caaggtgggtgaagatc
gagccccctgggctggccccccaccaaggccaagcgccgctggtgcagcgcgagaagcgcgcctg
accctgggcgccatgttccctgggcttccctgggcgcccggcagcaccatgggcgcccgcagcctg
accctgaccgtgcaggccccgcagctgctgagcggcatcgtgcagcagcagaacaacctgctgcgc
gccatcgaggccccagcagcacctgctgcagctgaccgtgtggggcatcaagcagctgcaggccccgc
gtgctggccgtggagcgctacctgaaggaccagcagctgctgggcatctggggctgcagcggcaag
ctgatctgcaccaccgcccgtgccctggaacgccagctggagcaacaagagcctggaccagatctgg
aacaacatgacctggatggagtgggagcgcgagatcgacaactacaccaacctgatctacacctg
atcgaggagagccagaaccagcaggagaagaacgagcaggagctgctggagctggacaagtgggccc
agcctgtggaactggttcgacatcagcaagtggctgtggtacatcaagatcttcatcatgatcgtg
ggcggccctggtgggcctgcgcacatcgtgttcaccgtgctgagcatcgtgaaccgcgtgcgccagggc
tacagccccctgagcttccagacccgcttccccgcccccccgcgccccgaaccgccccgaggggcatc
gaggaggagggcgggcgagcgcgaccgcgaccgcagcagccccctggtgcacggcctgctggccctg
atctgggacgacctgcgcagcctgtgcctgttcagctaccaccgctgcgcgauctgatcctgatc
gccgccccgcacatcgtggagctgctgggcgcgcgcggctgggaggccctgaagtactggggcaacctg
ctgcagtactggatccaggagctgaagaacagcgccgtgagcctgttcgacgccatcgccatcgcc
gtggccgagggcaccgaccgcatcatcgaggtggcccagcgcacatcgggcgcgccttccctgcacatc
ccccgcgcgcatccgccagggttcgagcgcgccttgcgtgaactcgag

FIG. 37

(SEQ ID NO:50)

49 / 131

gp120wtUS4

ACAACAGTCTTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGAAG
CAACCACCACTCTGTTTTGTGCATCAGATGCTAAAGCATACAAAGCAGAGGC
ACATAACGTCTGGGCTACACATGCCTGTGTACCCACAGACCCCAACCCACAG
GAAGTAAATTTAACAAATGTGACAGAAAATTTTAACATGTGGAAAAATAACA
TGGTGGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAGCCTAAA
GCCATGTGTAAAATTAACCCCACTCTGTGTTACTTTAAATTGTACTGATAAGT
TGACAGGTAGTACTAATGGCACAAATAGTACTAGTGGCACTAATAGTACTAG
TGGCACTAATAGTACTAGTACTAATAGTACTGATAGTTGGGAAAAGATGCCA
GAAGGAGAAATAAAAACTGCTCTTTCAATATCACCACAAGTGTAAGAGATA
AAGTGCAGAAAGAATATTCTCTCTTCTATAAACTTGATGTAGTACCAATAGAT
AATGATAATGCTAGCTATAGATTGATAAATTGTAATACCTCAGTCATTACACA
AGCCTGTCCAAAGGTATCTTTTGAACCAATTCCCATACATTATTGTGCCCCGG
CTGGTTTTGCGATTCTAAAGTGTAAGATAAGAAGTTCAATGGAACAGGACC
ATGTAAAAATGTCAGCACAGTACAATGCACACATGGAATTAGACCAGTAGTA
TCAACTCAACTGCTGTAAATGGCAGTCTAGCAGAAGAAGAGATAGTACTTA
GATCTGAAAATTTACAGACAATGCTAAAACCATAATAGTACAGCTGAATGA
ATCTGTAGAAATTAATTGTATAAGACCCAACAATAATACAAGAAAAAGTATA
CATATAGGACCAGGGAGAGCATTTTATGCAACAGGTGATATAATAGGAGACA
TAAGACAAGCACATTGTAACATTAGTAAAGCAAACCTGGACTAACACTTTAGA
ACAGATAGTTGAAAAATTAAGAGAACAAATTTGGGAATAATAAAACAATAATC
TTTAATTCATCCTCAGGAGGGGACCCAGAAATTGTATTTACAGTTTTAATTG
TGGAGGGGAATTTTTCTATTGTAATACATCACAACCTATTTAATAGTACCTGGA
ATATTACTGAAGAGGTAAATAAGACTAAAGAAAATGACACTATCATACTCCC
ATGCAGAATAAGACAAATTATAAACATGTGGCAAGAAGTAGGAAAAGCAAT
GTATGCCCTCCCATCAGAGGACAAATTAATGTTTCATCAAATATTACAGGG
CTGCTATTAAGTAGAGATGGTGGTACTAACAATAATAGGACGAACGACACCG
AGACCTTCAGACCTGGGGGAGGAAACATGAAGGACAATTGGAGAAGTGAAT
TATATAAATATAAAGTAGTAAGAATTGAACCATTAGGAGTAGCACCCACCCA
GGCAAAGAGAAGAGTGGTGCAAAGAGAGAAAAGA

FIG. 38

(SEQ ID NO:51)

50 / 131

gp140wtUS4

ACAACAGTCTTGTGGGTACAGTCTATTATGGGGTACCTGTGTGGAAAGAAG
CAACCACCACTCTGTTTTGTGCATCAGATGCTAAAGCATACAAAGCAGAGGC
ACATAACGTCTGGGCTACACATGCCTGTGTACCCACAGACCCCAACCCACAG
GAAGTAAATTTAACAAATGTGACAGAAAATTTAACATGTGGAAAAATAACA
TGGTGGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAGCCTAAA
GCCATGTGTAAAATTAACCCCACTCTGTGTTACTTTAAATTGTACTGATAAGT
TGACAGGTAGTACTAATGGCACAATAGTACTAGTGGCACTAATAGTACTAG
TGGCACTAATAGTACTAGTACTAATAGTACTGATAGTTGGGAAAAGATGCCA
GAAGGAGAAATAAAAACTGCTCTTTCAATATCACCACAAGTGTAAGAGATA
AAGTGCAGAAAGAATATTCTCTCTTCTATAAACTTGATGTAGTACCAATAGAT
AATGATAATGCTAGCTATAGATTGATAAATTGTAATACCTCAGTCATTACACA
AGCCTGTCCAAAGGTATCTTTGAACCAATTCCCATACATTATTGTGCCCCGG
CTGGTTTTGCGATTCTAAAGTGTAAGATAAGAAGTTCAATGGAACAGGACC
ATGTAAAAATGTCAGCACAGTACAATGCACACATGGAATTAGACCAGTAGTA
TCAACTCAACTGCTGTAAATGGCAGTCTAGCAGAAGAAGAGATAGTACTTA
GATCTGAAAATTTACAGACAATGCTAAAACCATAATAGTACAGCTGAATGA
ATCTGTAGAAATTAATTGTATAAGACCCAACAATAATACAAGAAAAAGTATA
CATATAGGACCAGGGAGAGCATTTTATGCAACAGGTGATATAATAGGAGACA
TAAGACAAGCACATTGTAACATTAGTAAAGCAAACCTGGACTAACACTTTAGA
ACAGATAGTTGAAAAATTAAGAGAACAATTTGGGAATAATAAAACAATAATC
TTTAATTCATCCTCAGGAGGGGACCCAGAAATTGTATTTACAGTTTTAATTG
TGGAGGGGAATTTTTCTATTGTAATACATCACAACCTATTTAATAGTACCTGGA
ATATTACTGAAGAGGTAAATAAGACTAAAGAAAATGACACTATCATACTCCC
ATGCAGAATAAGACAAATTATAAACATGTGGCAAGAAGTAGGAAAAGCAAT
GTATGCCCTCCCATCAGAGGACAAATTAAATGTTTCATCAAATATTACAGGG
CTGCTATTAAGTAGAGATGGTGGTACTAACAAATAATAGGACGAACGACACCG
AGACCTTCAGACCTGGGGGAGGAAACATGAAGGACAATTGGAGAAGTGAAT
TATATAAATATAAAGTAGTAAGAATTGAACCATTAGGAGTAGCACCCACCCA
GGCAAAGAGAAGAGTGGTGCAAAGAGAGAAAAGAGCAGTGGGACTAGGAG
CTTTGTTTATTGGGTTCTTGGGAGCAGCAGGAAGCACTATGGGCGCAGCGTC
AGTGACGCTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCAACAG
CAGAACAATTTGCTGAGAGCTATTGAGGCGCAACAGCATCTGTTGCAACTCA
CGGTCTGGGGCATCAAACAGCTCCAGGCAAGAATCCTGGCTGTGGAAAGATA
CCTAAAGGATCAACAGCTCCTAGGGATTTGGGGTTGCTCTGGAAAACCTATT
GCACCACTACTGTGCCTTGGAACCTAGTTGGAGTAATAAATCTCTGACTGAG
ATTTGGGATAATATGACCTGGATGGAGTGGGAAAGAGAAATTGGCAATTATA
CAGGCTTAATATACAATTTAATTGAAATAGCACAAAACCAGCAAGAAAAGAA
TGAACAAGAATTATTGGAATTAGACAAGTGGGCAAGTTTGTGGAATTGGTTT
GATATAACAACTGGCTGTGGTATATA

FIG. 39

(SEQ ID NO:52)

51 / 131

gp160wtUS4

ACAACAGTCTTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGAAG
CAACCACCACTCTGTTTTGTGCATCAGATGCTAAAGCATACAAAGCAGAGGC
ACATAACGTCTGGGCTACACATGCCTGTGTACCCACAGACCCCAACCCACAG
GAAGTAAATTTAACAAATGTGACAGAAAATTTTAACATGTGGAAAAATAACA
TGGTGGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAGCCTAAA
GCCATGTGTAAAATTAACCCCACTCTGTGTTACTTTAAATTGTACTGATAAGT
TGACAGGTAGTACTAATGGCACAATAAGTACTAGTGGCACTAATAGTACTAG
TGGCACTAATAGTACTAGTACTAATAGTACTGATAGTTGGGAAAAGATGCCA
GAAGGAGAAATAAAAAACTGCTCTTTCAATATCACCACAAGTGTAAGAGATA
AAGTGCAGAAAGAATATTCTCTCTTCTATAAACTTGATGTAGTACCAATAGAT
AATGATAATGCTAGCTATAGATTGATAAATTGTAATACCTCAGTCATTACACA
AGCCTGTCCAAAGGTATCTTTTGAACCAATTCCTACATATTATTGTGCCCCGG
CTGGTTTTTGCATTCTAAAGTGTAAGATAAGAAGTTCAATGGAACAGGACC
ATGTAAAAATGTCAGCACAGTACAATGCACACATGGAATTAGACCAGTAGTA
TCAACTCAACTGCTGTAAATGGCAGTCTAGCAGAAGAAGAGATAGTACTTA
GATCTGAAAATTTACAGACAATGCTAAAACCATAATAGTACAGCTGAATGA
ATCTGTAGAAATTAATTGTATAAGACCCAACAATAACAAGAAAAAGTATA
CATATAGGACCAGGGAGAGCATTATGCAACAGGTGATATAATAGGAGACA
TAAGACAAGCACATTGTAACATTAGTAAAGCAAACCTGGACTAACACTTTAGA
ACAGATAGTTGAAAAATTAAGAGAACAATTTGGGAATAATAAAACAATAATC
TTTAATTCATCCTCAGGAGGGGACCCAGAAATTGTATTTACAGTTTTTAATTG
TGGAGGGGAATTTTTCTATTGTAATACATCACAACCTATTTAATAGTACCTGGA
ATATTACTGAAGAGGTAAATAAGACTAAAGAAAATGACACTATCATACTCCC
ATGCAGAATAAGACAAATTATAAACATGTGGCAAGAAGTAGGAAAAGCAAT
GTATGCCCCCTCCCATCAGAGGACAAATTAAATGTTCATCAAATATTACAGGG
CTGCTATTAAGTATAGAGATGGTGGTACTAACAATAATAGGACGAACGACACCG
AGACCTTCAGACCTGGGGGAGGAAACATGAAGGACAATTGGAGAAGTGAAT
TATATAAATATAAAGTAGTAAGAATTGAACCATTAGGAGTAGCACCCACCCA
GGCAAAGAGAAGAGTGGTGCAAAGAGAGAAAAGAGCAGTGGGACTAGGAG
CTTTGTTTCATTGGGTTCTTGGGAGCAGCAGGAAGCACTATGGGCGCAGCGTC
AGTGACGCTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCAACAG
CAGAACAATTTGCTGAGAGCTATTGAGGCGCAACAGCATCTGTTGCAACTCA
CGGTCTGGGGCATCAAACAGCTCCAGGCAAGAATCCTGGCTGTGGAAAGATA
CCTAAAGGATCAACAGCTCCTAGGGATTTGGGGTTGCTCTGGAAAACCTCATT
GCACCACTACTGTGCCTTGGAACTCTAGTTGGAGTAATAAATCTCTGACTGAG
ATTTGGGATAATATGACCTGGATGGAGTGGGAAAGAGAAATTGGCAATTATA
CAGGCTTAATATACAATTTAATTGAAATAGCACAAAACCAGCAAGAAAAGAA
TGAACAAGAATTATTGGAATTAGACAAGTGGGCAAGTTTGTGGAATTGGTTT
GATATAACAACTGGCTGTGGTATATAAGAATATTCATAATGATAGTAGGAG
GCTTGATAGGTTTAAGAATAGTTTTTGTGTACTTTCTATAGTGAATAGAGTT
AGGCAGGGATACTACCAATATCATTGCAGACCCGCCTCCAGCTCAGAGGG

FIG. 40A

(SEQ ID NO:53)

52 / 131

GACCCGACAGGCCCGAAGGAATCGAAGAAGAAGGTGGAGAGAGAGACAGA
GACAGATCCAATCGATTAGTGCATGGATTATTGGCACTCATCTGGGACGATCT
GCGGAGCCTGTGCCTCTTCAGCTACCAACCGCTTGAGAGACTTACTCTTGATTG
TAGCGAGGATTGTGGAACCTTCTGGGACGCAGGGGGTGGGAAGCCCTCAAGTA
TTGGTGGAATCTCCTGCAGTATTGGAGTCAGGAGCTAAAGAGTAGTGCTGTT
AGTTTGTTTAATGCCACAGCAATAGCAGTAGCTGAAGGGACAGATAGGATTA
TAGAAATAGTACAAAGAATTTTTAGAGCTGTAATTCACATACCTAGAAGAAT
AAGACAGGGCTTGGAGAGGGCTTTACTATAA

FIG. 40B
(SEQ ID NO:53)

53 / 131

gp120.modUS4

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGGAGCA
GTCTTCGTTTTGCCCCAGCGCCACCACCGTGCTGTGGGTGACCGTGTAACGCGGTGCCCGTG
TGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCTTACAAGGCCGAGGC
CCACAACGTGTGGGCCACCCACGCCTGCGTGCCACCGACCCCAACCCCCAGGAGGTGAACC
TGACCAACGTGACCGAGAACTTCAACATGTGGAAGAACATGGTGGAGCAGATGCATGAG
GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTG
ACCCTGAACTGCACCGACAAGCTGACCGGCAGCACCAACGGCACCAACAGCACCAGCGGCAC
CAACGACACCAGCGGCACCAACAGCACCAGCACCAACAGCACCAGACAGCTGGGAGAAGATG
CCCGAGGGCGAGATCAAGAACTGCAGCTTCAACATCACCACCAGCGTGCGCGACAAGGTGCA
GAAGGAGTACAGCCTGTTCTACAAGCTGGACGTGGTGCCCATCGACAACGACAACGCCAGCT
ACCGCCTGATCAACTGCAACACCAGCGTGATCACCAGGCCTGCCCAAGGTGAGCTTCGAGC
CCATCCCCATCCACTACTGCGCCCCCGCCGGCTTCGCCATCCTGAAGTGCAAGGACAAGAAGT
TCAACGGCACCCGGCCCCCTGCAAGAACGTGAGCACCGTGCAAGTGCAACCCACGGCATCCGCCCC
GTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGAGATCGTGCTGCGCTC
CGAGAACTTCACCGACAACGCCAAGACCATCATCGTGCAAGCTGAACGAGTCCGTGGAGATCA
ACTGCATCCGCCCCAACAACAACACGCGTAAGAGCATCCACATCGGCCCCCGCCGCGCCTTCT
ACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCAAGGCCAAC
TGGACCAACACCCTCGAGCAGATCGTGGAGAAGCTGCGCGAGCAGTTCCGGCAACAACAAGAC
CATCATCTTCAACAGCAGCAGCGGCGGCGACCCCGAGATCGTGTTCCAAGCTTCAACTGCGG
CGGCGAGTTCTTCTACTGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCACCGAGGA
GGTGAACAAGACCAAGGAGAACGACACCATCATCCTGCCCTGCCGATCCGCCAGATCATCA
ACATGTGGCAGGAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCCAGATCAAGTGC
AGCAGCAATATTACCGGCCTGCTGCTGACCCGCGACGGCGGCACCAACAACAACCGCACCAA
CGACACCGAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAACCTGGCGCAGCGAGCTGT
ACAAGTACAAGGTGGTGCGCATCGAGCCCCTGGGCGTGCCCCCACCCAGGCCAAGCGCCGC
GTGGTGCAAGCGGAGAAAGCGCTAAGATATCGGATCCTCTAGA

FIG. 41
(SEQ ID NO:54)

54 / 131

gp120.mod.US4.del128-194

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGG
AGCAGTCTTCGTTTCGCCCAGCGCCACCACCGTGCTGTGGGTGACCGTGTA CTACGGCG
TGCCCGTGTGGAAGGAGGCCACCACCACCCTGTTCTGCGCCAGCGACGCCAAGGCTTAC
AAGGCCGAGGCCCAACGTGTGGGCCACCCACGCCTGCGTGCCCAACGACCCCAACCC
CCAGGAGGTGAACCTGACCAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGG
TGGAGCAGATGCATGAGGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTG
AAGCTGACCCCCCTGTGCGTGGGGGCAGGGAACTGCGGAGACCAGCGTGATCACCAGGC
CTGCCCCAAGGTGAGCTTCGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTTCG
CCATCCTGAAGTGCAAGGACAAGAAGTTCAACGGCACCGGCCCCCTGCAAGAACGTGAGC
ACCGTGCAAGTGACCCACGGCATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGG
CAGCCTGGCCGAGGAGGAGATCGTGCTGCGCTCCGAGAACTTCACCGACAACGCCAAGA
CCATCATCGTGCAAGTGAACGAGTCCGTGGAGATCAACTGCATCCGCCCCAACAACAAC
ACGCGTAAGAGCATCCACATCGGCCCCGGCCGCGCCTTCTACGCCACCGGCGACATCAT
CGGCGACATCCGCCAGGCCCACTGCAACATCAGCAAGGCCAACTGGACCAACACCCTCG
AGCAGATCGTGGAAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGACCATCATCTTCAAC
AGCAGCAGCGGCGGCGACCCCGAGATCGTGTTCCACAGCTTCAACTGCGGCGGCGAGTT
CTTCTACTGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCACCAGGAGGTGA
ACAAGACCAAGGAGAACGACACCATCATCCTGCCCTGCCGCATCCGCCAGATCATCAAC
ATGTGGCAGGAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCCAGATCAAGTG
CAGCAGCAATATTACCGGCCTGCTGCTGACCCGCGACGGCGGCACCAACAACAACCGCA
CCAACGACACCGAGACCTTCCGCCCCGGCGGGCAACATGAAGGACAACCTGGCGCAGC
GAGCTGTACAAGTACAAGGTGGTGCGCATCGAGCCCCTGGGCGTGGCCCCCACCAGGC
CAAGCGCCGCGTGGTGAGCGCGAGAAGCGCTAAGATATCGGATCCTCTAGA

FIG. 42

(SEQ ID NO:55)

55 / 131

gp140.modUS4

GAATTCGCCACCATGGATGCAATGAAGAGAGGGGCTCTGCTGTGTGCTGCTGCTGTGTGGAGCA
GTCTTCGTTTCGCCCAGCGCCACCAACCGTGCTGTGGGTGACCGTGTAACGCGTGCCCGTG
TGGAAGGAGGCCACCAACACCTGTTCTGCGCCAGCGACGCCAAGGCTTACAAGGCCGAGGC
CCACAACGTGTGGGCCACCCACGCCTGCGTGCCCAACCGACCCCAACCCCCAGGAGGTGAACC
TGACCAACGTGACCGAGAACTTCAACATGTGGAAGAAACAACATGGTGGAGCAGATGCATGAG
GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTG
ACCCTGAACTGCACCGACAAGCTGACCGGCAGCACCAACGGCACCAACAGCACCGACGCGGCAC
CAACAGCACCGCGGCACCAACAGCACCGACCAACAGCACCGACAGCTGGGAGAAGATG
CCCGAGGGCGAGATCAAGAACTGCAGCTTCAACATCACCACCAGCGTGCGCGACAAGGTGCA
GAAGGAGTACAGCCTGTTCTACAAGCTGGACGTGGTGCCCATCGACAACGACAACGCCAGCT
ACCGCCTGATCAACTGCAACACCAGCGTGATCACCAGGCCCTGCCCAAGGTGAGCTTCGAGC
CCATCCCCATCCACTACTGCGCCCCCGCGGCTTCGCCATCCTGAAGTGCAAGGACAAGAAGT
TCAACGGCACCGGCCCCCTGCAAGAAGCTGAGCACCGTGCAAGTGCACCCACGGCATCCGCCCC
GTGGTGAGCACCCAGCTGCTGAAACGGCAGCCTGGCCGAGGAGGAGATCGTGCTGCGCTC
CGAGAACTTCACCGACAACGCCAAGACCATCATCGTGACGCTGAACGAGTCCGTGGAGATCA
ACTGCATCCGCCCCAACAACAACACGCGTAAGAGCATCCACATCGGCCCGGCGCGCCTTCT
ACGCCACCGCGCATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCAAGGCCAAC
TGGACCAACACCCTCGAGCAGATCGTGGAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGAC
CATCATCTTCAACAGCAGCAGCGGCGGCGACCCGAGATCGTGTTCCACAGCTTCAACTGCGG
CGGCGAGTTCTTCTACTGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCACCGAGGA
GGTGAACAAAGACCAAGGAGAACGACACCATCATCCTGCCCTGCCGCAATCCGCCAGATCATCA
ACATGTGGCAGGAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCCAGATCAAGTGC
AGCAGCAATATTACCGGCCTGCTGCTGACCCGCGACGGCGGCACCAACAACAACCGCACCA
CGACACCGAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAACTGGCGCAGCGAGCTGT
ACAAGTACAAGGTGGTGCGCATCGAGCCCCTGGGCGTGGCCCCACCCAGGCCAAGCGCCG
GTGGTGACGCGGAGAAGCGCGCCGTGGGCGCTGGGCGCCCTGTTTCATCGGCTTCCTGGGCGCC
GCCGGGAGCACCATGGGCGCCGCTCCGTGACCCTGACCGTGACGGCCCGCCAGCTGCTGAG
CGGCATCGTGACGAGCAGAAACAACCTGCTGCGCGCCATCGAGGCCAGCAGCACCTGCTGC
AGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCATCCTGGCCGTGGAGCGCTACCTG
AAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCACCGT
GCCCTGGAACAGCAGCTGGAGCAACAAGAGCCTGACCGAGATCTGGGACAACATGACCTGGA
TGGAGTGGGAGCGCGAGATCGGCAACTACCGGCCTGATCTAACCTGATCGAGATCGCC
CAGAACCAGCAGGAGAAGAAGCAGGAGCTGCTGGAGCTGGACAAGTGGGCCAGCCTGT
GGAAGTGGTTCGACATCACCAACTGGCTGTGGTACATCTAAGATATCGGATCCTCTAGA

FIG. 43

(SEQ ID NO:56)

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GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGGAGCA
GTCTTCGTTTCGCCCAGCGCCACCACCGTGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTG
TGGAAGGAGGCCACCACCACCCTGTTCTGCGCCAGCGACGCCAAGGCTTACAAGGCCGAGGC
CCACAACGTGTGGGCCACCCACGCCTGCGTGCCACCGACCCCAACCCCCAGGAGGTGAACC
TGACCAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCATGAG
GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTG
ACCCTGAACTGCACCGACAAGCTGACCGGCAGCACCAACGGCACCAACAGCACCAGCGGCAC
CAACAGCACCGCGCACCAACAGCACCAGCACCAACAGCACCAGCAGCTGGGAGAAGATG
CCCGAGGGCGAGATCAAGAACTGCAGCTTCAACATCACCACCAGCGTGCGCGACAAGGTGCA
GAAGGAGTACAGCCTGTTCTACAAGCTGGACGTGGTGCCCATCGACAACGACAACGCCAGCT
ACCGCCTGATCAACTGCAACACCAGCGTGATCACCAGGCCTGCCCAAGGTGAGCTTCGAGC
CCATCCCCATCCACTACTGCGCCCCCGCCGGCTTCGCCATCCTGAAGTGCAAGGACAAGAAGT
TCAACGGCACCGGCCCTGCAAGAACGTGAGCACCGTGACGTGCAGTGACCCACGGCATCCGCCCC
GTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGAGATCGTGCTGCGCTC
CGAGAACTTCACCGACAACGCCAAGACCATCATCGTGACGTGAACGAGTCCGTGGAGATCA
ACTGCATCCGCCCCAACAACAACACGCGTAAGAGCATCCACATCGGCCCCGGCCGCGCCTTCT
ACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCAAGGCCAAC
TGGACCAACACCCTCGAGCAGATCGTGGAGAAGCTGCGCGAGCAGTTCCGGCAACAACAAGAC
CATCATCTTCAACAGCAGCAGCGGCGGCGACCCCGAGATCGTGTTCCACAGCTTCAACTGCGG
CGGCGAGTTCTTCTACTGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCACCGAGGA
GGTGAACAAGACCAAGGAGAACGACACCATCATCCTGCCCTGCCGCA TCCGCCAGATCATCA
ACATGTGGCAGGAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCCAGATCAAGTGC
AGCAGCAATATTACCGGCCTGCTGCTGACCCGCGACGGCGGCACCAACAACAACCGCACCA
CGACACCGAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAACCTGGCGCAGCGAGCTGT
ACAAGTACAAGGTGGTGCGCATCGAGCCCCCTGGGCGTGCCCCCAACAGGCCAAGCGCCGC
GTGGTGACGCGGAGAAGAGCGCCCTGGGCCTGGGCGCCCTGTTTCATCGGCTTCTTGGGCGCC
GCCGGGAGCACCATGGGCGCCGCTCCGTGACCCTGACCGTGACAGGCCCGCCAGCTGCTGAG
CGGCATCGTGACAGCAGCAGAACAACCTGCTGCGCGCCATCGAGGCCAGCAGCACCTGCTGC
AGCTGACCGTGTTGGGCGATCAAGCAGCTGCAGGCCCGCATCCTGGCCGTGGAGCGCTACCTG
AAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCACCGT
GCCCTGGAACAGCAGCTGGAGCAACAAGAGCCTGACCGAGATCTGGGACAACATGACCTGGA
TGGAGTGGGAGCGGAGATCGGCAACTACACCGGCCTGATCTACAACCTGATCGAGATCGCC
CAGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAAGTGGGCCAGCCTGT
GGAAGTGGTTCGACATCACCAACTGGCTGTGGTACATCTAAGATATCGGATCCTCTAGA

FIG. 44

(SEQ ID NO:57)

57 / 131

gp140.TM.modUS4

GAATTGCGCCACCATGGATGCAATGAAGAGAGGGGCTCTGCTGTGTGCTGCTGCTGTGTGGAGCA
GTCTTCGTTTCGCCCAGCGCCACCAACCGTGCTGTGGGTGACCGTGTAACGCGTGCCCGTG
TGGAAGGAGGCCACCAACACCTGTTCTGCGCCAGCGACGCCAAGGCTTACAAGGCCGAGGC
CCACAACGTGTGGGCCACCCACGCCTGCGTGCCACCGACCCCAACCCCCAGGAGGTGAACC
TGACCAACGTGACCGAGAATTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCATGAG
GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTG
ACCCTGAACTGCACCGACAAGCTGACCGGCAGCACCAACGGCACCAACAGCACCGAGCGGCAC
CAACAGCACCGCGGCACCAACAGCACCGAGCACCAACAGCACCGACAGCTGGGAGAAGATG
CCCGAGGGGCGAGATCAAGAACTGCAGCTTCAACATCACCACCGCGTGCGGACAAGGTGCA
GAAGGAGTACAGCCTGTTCTACAAGCTGGACGTGGTGCCCATCGACAACGACAACGCCAGCT
ACCGCCTGATCAACTGCAACACCGAGCGTGATCACCAGGCCTGCCCAAGGTGAGCTTCGAGC
CCATCCCCATCCACTACTGCGCCCCCGCGGCTTCGCCATCCTGAAGTGCAAGGACAAGAAGT
TCAACGGCACCGGCCCCCTGCAAGAACGTGAGCACCGTGCAAGTGCACCCACGGCATCCGCCCC
GTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGAGATCGTGCTGCGCTC
CGAGAACTTCACCGACAACGCCAAGACCATCATCTGTCAGCTGAACGAGTCCGTGGAGATCA
ACTGCATCCGCCCCAACAACAACACGCGTAAGAGCATCCACATCGGCCCCGGCCGCGCCTTCT
ACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCAAGGCCAAC
TGGACCAACACCCTCGAGCAGATCGTGGAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGAC
CATCATCTTCAACAGCAGCAGCGGCGGCGACCCCGAGATCGTGTTCCACAGCTTCAACTGCGG
CGGCGAGTTCTTCTACTGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCACCGAGGA
GGTGAACAAGACCAAGGAGAACGACACCATCATCCTGCCCTGCCGATCCGCCAGATCATCA
ACATGTGGCAGGAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCCAGATCAAGTGC
AGCAGCAATATTACCGGCCTGCTGCTGACCCGCGACGGCGGCACCAACAACAACCGCACCA
CGACACCGAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAACCTGGCGCAGCGAGCTGT
ACAAGTACAAGGTGGTGCGCATCGAGCCCCTGGGCGTGCCCCCACCCAGGCCAAGCGCCGC
GTGGTGCGAGCGCGAGAAGCGCGCCCTGGGCGCCCTGTTTCATCGGCTTCCTGGGCGCC
GCCGGGAGCACCATGGGCGCCGCTCCGTGACCCTGACCGTGCGAGGCCCGCCAGCTGCTGAG
CGGCATCGTGCGAGCAGCAGAACAACCTGCTGCGCGCCATCGAGGCCAGCAGCACCTGCTGC
AGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCATCCTGGCCGTGGAGCGCTACCTG
AAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCAACCGT
GCCCTGGAACAGCAGCTGGAGCAACAAGAGCCTGACCGAGATCTGGGACAACATGACCTGGA
TGGAGTGGGAGCGCGAGATCGGCAACTACACCGGCCTGATCTACAACCTGATCGAGATCGCC
CAGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAAGTGGGCCAGCCTGT
GGAACCTGGTTTCGACATCACTAAGTGGCTGTGGTACATCCGCATCTTCATCATGATCGTGGGCG
GCCTGATCGGCCTGCGCATCGTGTTCCCGTGCTGAGCATCGTGTAAGATATCGGATCCTCTA
GA

FIG. 45
(SEQ ID NO:58)

58 / 131

Gp140modUS4.DV1V2

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGC
TGTGTGGAGCAGTCTTCGTTTCGCCCAGCGCCACCACCGTGCTGTGGGTGACC
GTGTACTACGGCGTGCCCGTGTGGAAGGAGGCCACCACCACCCTGTTCTGCG
CCAGCGACGCCAAGGCTTACAAGGCCGAGGCCACAACGTGTGGGCCACCCA
CGCCTGCGTGCCACCGACCCCAACCCCAAGGAGGTGAACCTGACCAACGTG
ACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCATGAG
GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGGGCGCCGGCC
AGGCCTGCCCCAAGGTGAGCTTCGAGCCCATCCCCATCCACTACTGCGCCCC
CGCCGGCTTCGCCATCCTGAAGTGCAAGGACAAGAAGTTCAACGGCACCGGC
CCCTGCAAGAACGTGAGCACCGTGCAAGTGCAACCCACGGCATCCGCCCCGTGG
TGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGAGATCGTGCT
GCGCTCCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGCAAGTGAAC
GAGTCCGTGGAGATCAACTGCATCCGCCCCAACAACAACACGCGTAAGAGCA
TCCACATCGGCCCCGGCCGCGCCTTCTACGCCACCGGCGACATCATCGGCGA
CATCCGCCAGGCCCCACTGCAACATCAGCAAGGCCAACTGGACCAACACCCTC
GAGCAGATCGTGGAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGACCATC
ATCTTCAACAGCAGCAGCGGCGGCGACCCCGAGATCGTGTTCCACAGCTTCA
ACTGCGGCGGCGAGTTCTTCTACTGCAACACCAGCCAGCTGTTCAACAGCAC
CTGGAACATCACCGAGGAGGTGAACAAGACCAAGGAGAACGACACCATCAT
CCTGCCCTGCCGCATCCGCCAGATCATCAACATGTGGCAGGAGGTGGGCAAG
GCCATGTACGCCCCCCCCATCCGCGGCCAGATCAAGTGCAGCAGCAATATTA
CCGGCCTGCTGCTGACCCGCGACGGCGGCACCAACAACAACCGCACCAACGA
CACCGAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAACCTGGCGCAGC
GAGCTGTACAAGTACAAGGTGGTGCATCGAGCCCCTGGGCGTGGCCCCCA
CCCAGGCCAAGCGCCGCGTGGTGCAGCGGAGAAAGCGCGCCGTGGGCCTGG
GCGCCCTGTTTCATCGGCTTCCTGGGCGCCGCGGGAGCACCATGGGCGCCGC
CTCCGTGACCCTGACCGTGCAGGCCCGCCAGCTGCTGAGCGGCATCGTGCAAG
CAGCAGAACAACTGCTGCGCGCCATCGAGGCCAGCAGCACCTGCTGCAGC
TGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCATCCTGGCCGTGGAGCG
CTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTG
ATCTGCACCACCACCGTGCCCTGGAACAGCAGCTGGAGCAACAAGAGCCTGA
CCGAGATCTGGGACAACATGACCTGGATGGAGTGGGAGCGCGAGATCGGCA
ACTACACCGGCCTGATCTACAACCTGATCGAGATCGCCAGAACCAGCAGGA
GAAGAACGAGCAGGAGCTGCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAA
CTGGTTCGACATCACCAACTGGCTGTGGTACATCTAAGATATCGGATCCTCTA
GA

FIG. 46

(SEQ ID NO:59)

59 / 131

Gp140modUS4.DV2

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGC
TGTGTGGAGCAGTCTTCGTTTCGCCCAGCGCCACCACCGTGCTGTGGGTGACC
GTGTACTACGGCGTGCCCGTGTGGAAGGAGGCCACCACCACCCTGTTCTGCG
CCAGCGACGCCAAGGCTTACAAGGCCGAGGCCACAACGTGTGGGCCACCCA
CGCCTGCGTGCCACCGACCCCAACCCCAAGGAGGTGAACCTGACCAACGTG
ACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCATGAG
GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCC
CCCTGTGCGTGACCCTGAACTGCACCGACAAGCTGACCGGCAGCACCAACGG
CACCAACAGCACCGACCGCACCAACAGCACCGCGCACCAACAGCACCGAG
CACCAACAGCACCGACAGCTGGGAGAAGATGCCCCGAGGGCGAGATCAAGAA
CTGCAGCTTCAACATCGGCGCCGCGCCGCTGATCAACTGCAACACCAGCGTG
ATCACCCAGGCCTGCCCAAGGTGAGCTTCGAGCCCATCCCCATCCACTACT
GCGCCCCCGCCGGCTTCGCCATCCTGAAGTGCAAGGACAAGAAGTTCAACGG
CACCGGCCCTGCAAGAACGTGAGCACCGTGACGTGCACCCACGGCATCCGC
CCCGTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGAGA
TCGTGCTGCGTCCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGCA
GCTGAACGAGTCCGTGGAGATCAACTGCATCCGCCCCAACAACAACACGCGT
AAGAGCATCCACATCGGCCCGGCGCGCCTTCTACGCCACCGGCGACATCA
TCGGCGACATCCGCCAGGCCCACTGCAACATCAGCAAGGCCAACTGGACCAA
CACCTCGAGCAGATCGTGGAGAAGCTGCGCGAGCAGTTCGGCAACAACAA
GACCATCATCTTCAACAGCAGCAGCGGCGGCGACCCCGAGATCGTGTTCCAC
AGCTTCAACTGCGGCGGCGAGTTCTTCTACTGCAACACCAGCCAGCTGTTCAA
CAGCACCTGGAACATCACCGAGGAGGTGAACAAGACCAAGGAGAACGACAC
CATCATCCTGCCCTGCCGCATCCGCCAGATCATCAACATGTGGCAGGAGGTG
GGCAAGGCCATGTACGCCCCCCCCATCCGCGGCCAGATCAAGTGACGACGCA
ATATTACCGGCCTGCTGCTGACCCGCGACGGCGGCCACCAACAACAACCGCAC
CAACGACACCGAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAACCTG
GCGCAGCGAGCTGTACAAGTACAAGGTGGTGCGCATCGAGCCCCTGGGCGTG
GCCCCACCCAGGCCAAGCGCCGCGTGGTGACGCGCGAGAAGCGCGCCGTG
GGCCTGGGCGCCCTGTTTCATCGGCTTCTTGGGCGCCGCGGGAGCACCATGG
GCGCCGCTCCGTGACCCTGACCGTGACGGCCCGCCAGCTGCTGAGCGGCAT
CGTGACGACGAGAACAACCTGCTGCGCGCCATCGAGGCCAGCAGCACCTG
CTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCATCCTGGCCG
TGGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGG
CAAGCTGATCTGCACCACCACCGTGCCCTGGAACAGCAGCTGGAGCAACAAG
AGCCTGACCGAGATCTGGGACAACATGACCTGGATGGAGTGGGAGCGCGAG
ATCGGCAACTACACCGGCCTGATCTACAACCTGATCGAGATCGCCCAGAACC
AGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAAGTGGGCCAGCC
TGTGGAAGTGGTTCGACATCACCAACTGGCTGTGGTACATCTAAGATATCGG
ATCCTCTAGA

FIG. 47
(SEQ ID NO:60)

60 / 131

Gp140modmutUS4.DV1V2

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGC
TGTGTGGAGCAGTCTTCGTTTCGCCCAGCGCCACCACCGTGCTGTGGGTGACC
GTGTACTACGGCGTGCCCGTGTGGAAGGAGGCCACCACCACCTGTTCTGCG
CCAGCGACGCCAAGGCTTACAAGGCCGAGGCCCAACACGTGTGGGCCACCC
ACGCCTGCGTGCCACCGACCCCAACCCCCAGGAGGTGAACCTGACCAACGT
GACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCATGA
GGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGGGCGCCGGC
CAGGCCTGCCCCAAGGTGAGCTTCGAGCCCATCCCCATCCACTACTGCGCCC
CCGCCGGCTTCGCCATCCTGAAGTGCAAGGACAAGAAGTTCAACGGCACCGG
CCCCTGCAAGAACGTGAGCACCGTGCAAGTGCAACCCACGGCATCCGCCCCGTG
GTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGAGATCGTGC
TGCGCTCCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGAGCTGAA
CGAGTCCGTGGAGATCAACTGCATCCGCCCCAACAACAACACGCGTAAGAGC
ATCCACATCGGCCCCGGCCGCGCCTTCTACGCCACCGGCGACATCATCGGCG
ACATCCGCCAGGCCCACTGCAACATCAGCAAGGCCAACTGGACCAACACCCT
CGAGCAGATCGTGGAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGACCAT
CATCTTCAACAGCAGCAGCGGCGGCGACCCCGAGATCGTGTTCACAGCTTC
AACTGCGGCGGCGAGTTCTTCTACTGCAACACCAGCCAGCTGTTCAACAGCA
CCTGGAACATCACCGAGGAGGTGAACAAGACCAAGGAGAACGACACCATCA
TCCTGCCCTGCCGCATCCGCCAGATCATCAACATGTGGCAGGAGGTGGGCAA
GGCCATGTACGCCCCCCCCATCCGCGGCCAGATCAAGTGCAGCAGCAATATT
ACCGGCCTGCTGCTGACCCGCGACGGCGGCCACCAACAACAACCGCACCAACG
ACACCGAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAACCTGGCGCA
GCGAGCTGTACAAGTACAAGGTGGTGCGCATCGAGCCCCTGGGCGTGGCCCC
CACCCAGGCCAAGCGCCGCGTGGTGCAGCGCGAGAAGAGCGCCGTGGGCCT
GGGCGCCCTGTTTCATCGGCTTCCTGGGCGCCGCGGGAGCACCATGGGCGCC
GCCTCCGTGACCCTGACCGTGCAGGCCCGCCAGCTGCTGAGCGGCATCGTGC
AGCAGCAGAACAACTGCTGCGCGCCATCGAGGCCAGCAGCACCTGCTGCA
GCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCATCCTGGCCGTGGAG
CGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGC
TGATCTGCACCACCACCGTGCCCTGGAACAGCAGCTGGAGCAACAAGAGCCT
GACCGAGATCTGGGACAACATGACCTGGATGGAGTGGGAGCGCGAGATCGG
CAACTACACCGGCCTGATCTACAACCTGATCGAGATCGCCCAGAACCAGCAG
GAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAAGTGGGCCAGCCTGTGG
AACTGGTTCGACATCACCAACTGGCTGTGGTACATCTAAGATATCGGATCCTC
TAGA

FIG. 48

(SEQ ID NO:61)

61 / 131

gp140.mod.US4.del128-194

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGG
AGCAGTCTTTCGTTTCGCCCAGCGCCACCACCGTGCTGTGGGTGACCGTGTA CTACGGCG
TGCCCGTGTGGAAGGAGGCCACCACCACCCTGTTCTGCGCCAGCGACGCCAAGGCTTAC
AAGGCCGAGGCCCAACAGTGTGGGCCACCCACGCCTGCGTGCCACCGACCCCAACCC
CCAGGAGGTGAACCTGACCAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGG
TGGAGCAGATGCATGAGGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTG
AAGCTGACCCCCCTGTGCGTGGGGGCAGGGAACTGCGAGACCAGCGTGATCACCAGGC
CTGCCCCAAGGTGAGCTTCGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTTCG
CCATCCTGAAGTGCAAGGACAAGAAGTTCAACGGCACCCGGCCCCCTGCAAGAACGTGAGC
ACCGTGCAGTGCACCCACGGCATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGG
CAGCCTGGCCGAGGAGGAGATCGTGCTGCGCTCCGAGAACTTCACCGACAACGCCAAGA
CCATCATCGTGCACTGAACGAGTCCGTGGAGATCAACTGCATCCGCCCCAACAACAAC
ACGCGTAAGAGCATCCACATCGGCCCCGGCCGCGCCTTCTACGCCACCGGCGACATCAT
CGGCGACATCCGCCAGGCCCCACTGCAACATCAGCAAGGCCAACTGGACCAACACCCTCG
AGCAGATCGTGGAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGACCATCATCTTCAAC
AGCAGCAGCGGCGGCGACCCCGAGATCGTGTTCCACAGCTTCAACTGCGGCGGCGAGTT
CTTCTACTGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCACCGAGGAGGTGA
ACAAGACCAAGGAGAACGACACCATCATCCTGCCCTGCCGCATCCGCCAGATCATCAAC
ATGTGGCAGGAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCCAGATCAAGTG
CAGCAGCAATATTACCGGCCTGCTGCTGACCCGCGACGGCGGCACCAACAACAACCGCA
CCAACGACACCGAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAACCTGGCGCAGC
GAGCTGTACAAGTACAAGGTGGTGCGCATCGAGCCCCTGGGCGTGCCCCCACCAGGC
CAAGCGCCGCGTGGTGCA GCGCGAGAAGCGCGCCGTGGGCCTGGGCGCCCTGTTTCATCG
GCTTCCTGGGCGCCGCGGGGAGCACCATGGGCGCCGCTCCGTGACCCCTGACCGTG CAG
GCCCCG CAGCTGCTGAGCGGCATCGTG CAGCAGCAGAACACCTGCTGCGCGCCATCGA
GGCCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCA
TCCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGC
GGCAAGCTGATCTGCACCACCACCGTGCCCTGGAACAGCAGCTGGAGCAACAAGAGCCT
GACCGAGATCTGGGACAACATGACCTGGATGGAGTGGGAGCGCGAGATCGGCAACTACA
CCGGCCTGATCTACAACCTGATCGAGATCGCCAGAACAGCAGGAGAAGAACGAGCAG
GAGCTGCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAACCTGGTTCGACATCACCAACTG
GCTGTGGTACATCTAAGATATCGGATCCTCTAGA

FIG. 49

(SEQ ID NO:62)

62/131

gp140.mut.mod.US4.del128-194

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGG
AGCAGTCTTCGTTTCGCCCAGCGCCACCACCGTGCTGTGGGTGACCGTGTAACGCGC
TGCCCGTGTGGAAGGAGGCCACCACCACCCTGTTCTGCGCCAGCGACGCCAAGGCTTAC
AAGGCCGAGGCCCAACCGTGTGGGCCACCCACGCCTGCGTGCCACCGACCCCAACCC
CCAGGAGGTGAACCTGACCAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGG
TGGAGCAGATGCATGAGGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTG
AAGCTGACCCCCCTGTGCGTGGGGGAGGGAAGTGCAGAGACCAGCGTGATCACCAGGC
CTGCCCCAAGGTGAGCTTCGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTTCG
CCATCCTGAAGTGCAAGGACAAGAAGTTCAACGGCACCGGCCCTGCAAGAACGTGAGC
ACCGTGCAGTGCACCCACGGCATCCGCCCCGTGGTGAGCACCAGCTGCTGCTGAACGG
CAGCCTGGCCGAGGAGGAGATCGTGCTGCGCTCCGAGAACTTCACCGACAACGCCAAGA
CCATCATCGTGCAGCTGAACGAGTCCGTGGAGATCAACTGCATCCGCCCCAACAACAAC
ACGCGTAAGAGCATCCACATCGGCCCGGCCGCGCCTTCTACGCCACCGGCGACATCAT
CGGCGACATCCGCCAGGCCCCACTGCAACATCAGCAAGGCCAACTGGACCAACACCCTCG
AGCAGATCGTGGAAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGACCATCATCTTCAAC
AGCAGCAGCGGCGGCGACCCCGAGATCGTGTTCCACAGCTTCAACTGCGGCGGCGAGTT
CTTCTACTGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCACCAGGAGGTGA
ACAAGACCAAGGAGAACGACACCATCATCCTGCCCTGCCGCATCCGCCAGATCATCAAC
ATGTGGCAGGAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCCAGATCAAGTG
CAGCAGCAATATTACCGGCCTGCTGCTGACCCGCGACGGCGGCACCAACAACAACCGCA
CCAACGACACCGAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAACCTGGCGCAGC
GAGCTGTACAAGTACAAGGTGGTGCGCATCGAGCCCCTGGGCGTGCCCCCACCAGGC
CAAGCGCCGCGTGCTGAGCGCGAGAAGAGCGCCGTGGGCCTGGGCGCCCTGTTTCATCG
GCTTCCTGGGCGCCGCCGGGAGCACCATGGGCGCCGCTCCGTGACCCCTGACCGTGCGAG
GCCCCAGCAGCACCTGCTGAGCGGCATCGTGAGCAGCAGAACCAACCTGCTGCGCGCCATCGA
GGCCCAGCAGCACCTGCTGAGCTGACCGTGTTGGGGCATCAAGCAGCTGCAGGCCCGCA
TCCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGC
GGCAAGCTGATCTGCACCACCACCGTGCCCTGGAACAGCAGCTGGAGCAACAAGAGCCT
GACCGAGATCTGGGACAACATGACCTGGATGGAGTGGGAGCGCGAGATCGGCAACTACA
CCGGCCTGATCTACAACCTGATCGAGATCGCCCAGAACCAGCAGGAGAAGAACGAGCAG
GAGCTGCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAAGTGGTTCGACATCACCAACTG
GCTGTGGTACATCTAAGATATCGGATCCTCTAGA

FIG. 50

(SEQ ID NO:63)

63 / 131

gp160.modUS4

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGGAGCA
GTCTTCGTTTCGCCCAGCGCCACCACCGTGCTGTGGGTGACCGTGTAACGCGCTGCCCCGTG
TGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCTTACAAGGCCGAGGC
CCACAACGTGTGGGCCACCCACGCCTGCGTGCCACCGACCCCAACCCCCAGGAGGTGAACC
TGACCAACGTGACCGAGAACTTCAACATGTGGAAGAACACATGGTGGAGCAGATGCATGAG
GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTG
ACCCTGAACTGCACCGACAAGCTGACCGGCAGCACCAACGGCACCAACAGCACCAGCGGCAC
CAACAGCACCAGCGGCACCAACAGCACCAGCACCAACAGCACCAGCAGCTGGGAGAAGATG
CCCGAGGGCGAGATCAAGAACTGCAGCTTCAACATCACCACCAGCGTGCGCGACAAGGTGCA
GAAGGAGTACAGCCTGTTCTACAAGCTGGACGTGGTGCCCATCGACAACGACAACGCCAGCT
ACCGCCTGATCAACTGCAACACCAGCGTGATCACCAGGCCTGCCCAAGGTGAGCTTCGAGC
CCATCCCCATCCACTACTGCGCCCCCGCGGCTTCGCCATCCTGAAGTGCAAGGACAAGAAGT
TCAACGGCACCGGCCCCCTGCAAGAACGTGAGCACCGTGCAAGTGCAACCCACGGCATCCGCCCC
GTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGAGATCGTGCTGCGCTC
CGAGAACTTCACCGACAACGCCAAGACCATCATCGTGCAAGCTGAACGAGTCCGTGGAGATCA
ACTGCATCCGCCCCAACAACAACACGCGTAAGAGCATCCACATCGGCCCCGGCCGCGCCTTCT
ACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCAAGGCCAAC
TGGACCAACACCCTCGAGCAGATCGTGGAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGAC
CATCATCTTCAACAGCAGCAGCGGCGGCGACCCCGAGATCGTGTTCCAAGCTTCAACTGCGG
CGGCGAGTTCTTCTACTGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCACCGAGGA
GGTGAACAAGACCAAGGAGAACGACACCATCATCCTGCCCTGCCGATCCGCCAGATCATCA
ACATGTGGCAGGAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCCAGATCAAGTGC
AGCAGCAATATTACCGCCCTGCTGCTGACCCGCGACGGCGGCACCAACAACACCGCACCA
CGACACCGAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAACCTGGCGCAGCGAGCTGT
ACAAGTACAGAGGTGGTGCGCATCGAGCCCCTGGGCGTGGCCCCCACCAGGCCAAGCGCCGC
GTGGTGACGCGGAGAAGCGCGCCGTGGGCTGGGCGCCCTGTTATCGGCTTCCTGGGCGCC
GCCGGGAGACCATGGGCGCCGCTCCGTGACCCTGACCGTGCAAGGCCCGCCAGCTGCTGAG
CGGCATCGTGACGAGCAGACAACCTGCTGCGCGCCATCGAGGCCAGCAGCACCTGCTGC
AGCTGACCGTGTTGGGCATCAAGCAGCTGCAGGCCCGCATCCTGGCCGTGGAGCGCTACCTG
AAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCAACCGT
GCCCTGGAACAGCAGCTGGAGCAACAAGAGCCTGACCGAGATCTGGGACAACATGACCTGGA
TGGAGTGGGAGCGCGAGATCGGCAACTACACCGGCCTGATCTACAACCTGATCGAGATCGCC
CAGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAAGTGGGCCAGCCTGT
GGAACTGGTTCGACATCACCAACTGGCTGTGGTACATCCGCATCTTCATCATGATCGTGGGCG
GCCTGATCGGCCTGCGCATCGTGTTCCGCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCT
ACAGCCCCATCAGCCTGCAGACCCGCCTGCCCCGCCAGCGCGGCCCCGACCGCCCCGAGGGC
ATCGAGGAGGAGGGCGGCGAGCGGACCGCGACCGCAGCAACCGCCTGGTGCACGGCCTGCT
GGCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTCACTACCAACCGCCTGCGCGACCT
GCTGCTGATCGTGGCCCGCATCGTGGAGCTGCTGGGCCCGCGCGCTGGGAGGCCCTGAAGT
ACTGGTGGAACCTGCTGCAGTACTGGAGCCAGGAGCTGAAGAGCAGCGCCGTGAGCCTGTT
AACGCCACCGCCATCGCCGTGGCCGAGGGCACCGACCGCATCATCGAGATCGTGACGCGCAT
CTTCCGCGCCGTGATCCACATCCCCCGCCGATCCGCCAGGGCCTGGAGCGCGCCCTGCTGTA
AGATATCGGATCCTCTAGA

FIG. 51
(SEQ ID NO:64)

64 / 131

gp160.modUS4.delV1

GAATTCGCCACCATGGATGCAATGAAGAGAGGGGCTCTGCTGTGTGCTGCTGCTGTGTGGAGCA
GTCTTCGTTTCGCCCAGCGCCACCACCGTGCTGTGGGTGACCGTGTAACGCGTGCCCGTG
TGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCTTACAAGGCCGAGGC
CCACAACGTGTGGGCCACCCACGCTGCGTGCCACCGACCCCAACCCCCAGGAGGTGAACC
TGACCAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCATGAG
GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTG
ACCCTGAACTGCACCGACAAGCTGGGCGCCGGCGGCGAGATCAAGAACTGCAGCTTCAACAT
CACCACCAGCGTGCGCGACAAGGTGCAGAAGGAGTACAGCCTGTTCTACAAGCTGGACGTGG
TGCCCATCGACAACGACAACGCCAGCTACCGCCTGATCAACTGCAACACCAGCGTGATCACCC
AGGCCTGCCCCAAGGTGAGCTTCGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTTCG
CCATCCTGAAGTGCAAGGACAAGAAGTTCAACGGCACCGGCCCTGCAAGAACGTGAGCACC
GTGCAGTGCACCACGGCATCCGCCCCGTGGTGAGCACCAGCTGCTGCTGAACGGCAGCCTG
GCCGAGGAGGAGATCGTGCTGCGCTCCGAGAACTTCACCGACAACGCCAAGACCATCATCGT
GCAGCTGAACGAGTCCGTGGAGATCAACTGCATCCGCCCCAACAACAACACGCGTAAGAGCA
TCCACATCGGCCCGCGCCGCGCCTTCTACGCCACCGGCGACATCATCGGCGACATCCGCCAGG
CCCACTGCAACATCAGCAAGGCCAACTGGACCAACACCCTCGAGCAGATCGTGGAGAAGCTG
CGCGAGCAGTTCGGCAACAACAAGACCATCATCTTCAACAGCAGCAGCGGCGGCGACCCCGA
GATCGTGTTCCACAGCTTCAACTGCGGCGGCGAGTTCTTCTACTGCAACACCAGCCAGCTGTT
CAACAGCACCTGGAACATCACCGAGGAGGTGAACAAGACCAAGGAGAACGACACCATCATCG
TGCCCTGCCGCATCCGCCAGATCATCAACATGTGGCAGGAGGTGGGCAAGGCCATGTACGCC
CCCCCATCCGCGGCCAGATCAAGTGACGAGCAATATTACCGGCCTGCTGCTGACCCGCGAC
GGCGGCACCAACAACAACCGCACCAACGACACCGAGACCTTCCGCCCCGCGGCGGCAACAT
GAAGGACAACCTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGCGCATCGAGCCCCCTGGGCG
TGGCCCCCAACCAGGCCAAGCGCCGCGTGGTGACGCGGAGAGCGCGCCGTGGGCCTGGGC
GCCCTGTTTCATCGGCTTCTTGGGCGCCGCGGAGCACCATGGGCGCCGCTCCGTGACCCCTG
ACCGTGCAAGGCCCGCCAGCTGCTGAGCGGCATCGTGACGAGCAGAGAACAACCTGCTGCGCGC
CATCGAGGCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCC
GCATCCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGC
GGCAAGCTGATCTGCACCACCACCGTGCCCTGGAACAGCAGCTGGAGCAACAAGAGCCTGAC
CGAGATCTGGGACAACATGACCTGGATGGAGTGGGAGCGCGAGATCGGCAACTACACCGGCC
TGATCTACAACCTGATCGAGATCGCCCAGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTG
GAGCTGGACAAGTGGGCCAGCCTGTGGAACCTGGTTTCGACATCACCACCTGGCTGTGGTACATC
CGCATCTTCATCATGATCGTGGGCGGCCTGATCGGCCTGCGCATCGTGTTCCCGGTGCTGAGC
ATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCATCAGCCTGCAGACCCGCTGCCCGCCAG
CGCGGCCCGACCGCCCCGAGGGCATCGAGGAGGAGGGCGGCGAGCGCGACCGCGACCGCA
GCAACCGCCTGGTGACGGCCTGCTGGCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGT
TCAGCTACCACCGCCTGCGCGACCTGCTGCTGATCGTGGCCCGCATCGTGGAGCTGCTGGGCC
GCCGCGGCTGGGAGGCCCTGAAGTACTGGTGGAACTGCTGCAGTACTGGAGCCAGGAGCTG
AAGAGCAGCGCCGTGAGCCTGTTCAACGCCACCGCCATCGCCGTGGCCGAGGGCACCGACCG
CATCATCGAGATCGTGACGCGCATCTTCCGCGCCGTGATCCACATCCCCCGCCGCATCCGCCA
GGGCCTGGAGCGCGCCCTGCTGTAAGATATCGGATCCTCTAGA

FIG. 52

(SEQ ID NO:65)

65/131

gp160.mod.US4.delV2

GAATTTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGG
AGCAGTCTTCGTTTCGCCACGCCACCACCGTGCTGTGGGTGACCGTGTAACGCGC
TGCCCGTGTGGAAGGAGGCCACCACCACCCTGTTCTGCGCCAGCGACGCCAAGGCTTAC
AAGGCCGAGGCCCAACGTGTGGGCCACCCACGCCTGCGTGCCACCGACCCCAACCC
CCAGGAGGTGAACCTGACCAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGG
TGGAGCAGATGCATGAGGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTG
AAGCTGACCCCCCTGTGCGTGACCCTGAACTGCACCGACAAGCTGACCGGCAGCACCA
CGGCACCAACAGCACCAGCGGCACCAACAGCACCAGCGGCACCAACAGCACCAGCACCA
ACAGCACCAGCAGCTGGGAGAAGATGCCCCGAGGGCGAGATCAAGAACTGCAGCTTCAAC
ATCGGCGCCGCGCCGCTGATCAACTGCAACACCAGCGTGATCACCCAGGCCTGCCCCAA
GGTGAGCTTCGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTTCGCCATCCTGA
AGTGCAAGGACAAGAAGTTCAACGGCACCGGCCCTGCAAGAACGTGAGCACCGTGCGAG
TGCACCCACGGCATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGC
CGAGGAGGAGATCGTGCTGCGCTCCGAGAACTTCACCGACAACGCCAAGACCATCATCG
TGCAGCTGAACGAGTCCGTGGAGATCAACTGCATCCGCCCCAACAAACAACACGCGTAAG
AGCATCCACATCGGCCCCGGCCGCGCCTTCTACGCCACCGGCGACATCATCGGCGACAT
CCGCCAGGCCCACTGCAACATCAGCAAGGCCAACTGGACCAACACCCTCGAGCAGATCG
TGGAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGACCATCATCTTCAACAGCAGCAGC
GGCGGCGACCCCGAGATCGTGTTCCACAGCTTCAACTGCGGCGGCGAGTTCTTCTACTG
CAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCACCGAGGAGGTGAACAAGACCA
AGGAGAACGACACCATCATCCTGCCCTGCCGCATCCGCCAGATCATCAACATGTGGCAG
GAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCCAGATCAAGTGCGAGCAGCAA
TATTACCGGCCTGCTGCTGACCCGCGACGGCGGCACCAACAACAACCGCACCAACGACA
CCGAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAACTGGCGCAGCGAGCTGTAC
AAGTACAAGGTGGTGCGCATCGAGCCCCCTGGGCGTGCGCCCCACCCAGGCCAAGCGCCG
CGTGGTGCGAGCGCGAGAAGCGCGCCGTGGGCCTGGGCGCCCTGTTTCATCGGCTTCCTGG
GCGCCGCGGGAGCACCATGGGCGCCGCTCCGTGACCCTGACCGTGCGAGGCCCGCCAG
CTGCTGAGCGGCATCGTGCGAGCAGCAGAACACCTGCTGCGCGCCATCGAGGCCAGCA
GCACCTGCTGCGAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCATCCTGGCCG
TGGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTG
ATCTGCACCACCACCGTGCCCTGGAACAGCAGCTGGAGCAACAAGAGCCTGACCGAGAT
CTGGGACAACATGACCTGGATGGAGTGGGAGCGCGAGATCGGCAACTACACCGGCCTGA
TCTACAACCTGATCGAGATCGCCCAGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTG
GAGCTGGACAAGTGGGCCAGCCTGTGGAACCTGGTTTCGACATCACCAACTGGCTGTGGTA
CATCCGCATCTTCATCATGATCGTGGGCGGCCTGATCGGCCTGCGCATCGTGTTCCGCCG
TGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCATCAGCCTGCAGACCCGC
CTGCCCCGCCAGCGCGGCCCGACCGCCCCGAGGGCATCGAGGAGGAGGGCGGCGAGCG
CGACCGCGACCGCAGCAACCGCCTGGTGCACGGCCTGCTGGCCCTGATCTGGGACGACC
TGCGCAGCCTGTGCCTGTTACGCTACCACCGCCTGCGCGACCTGCTGCTGATCGTGGCC
CGCATCGTGGAGCTGCTGGGCCGCGCGGCTGGGAGGCCCTGAAGTACTGGTGGAACCT
GCTGCAGTACTGGAGCCAGGAGCTGAAGAGCAGCGCCGTGAGCCTGTTCAACGCCACCG
CCATCGCCGTGGCCGAGGGCACCGACCGCATCATCGAGATCGTGCAGCGCATCTTCCGC
GCCGTGATCCACATCCCCCGCGCATCCGCCAGGGCCTGGAGCGCGCCCTGCTGTAAGA
TATCGGATCCTCTAGA

FIG. 53

(SEQ ID NO:66)

SUBSTITUTE SHEET (RULE 26)

66 / 131

gp160.modUS4delV1/2

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGGAGCA
GTCTTCGTTTTGCCCCAGCGCCACCACCGTGCTGTGGGTGACCGTGACTACGGCGTGCCCGTG
TGGAAGGAGGCCACCACCACCCTGTTCTGCGCCAGCGACGCCAAGGCTTACAAGGCCGAGGC
CCACAACGTGTGGGCCACCCACGCCTGCGTGCCCAACGCCAACCCCCAGGAGGTGAACC
TGACCAACGTGACCGAGAACTTCAACATGTGGAAGAACATGGTGGAGCAGATGCATGAG
GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGGGCGCCGGCCAGGCCTGCCC
CAAGGTGAGCTTCGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTTCGCCATCCTGAA
GTGCAAGGACAAGAAGTTCAACGGCACCGGCCCTGCAAGAACGTGAGCACCGTGCAGTGCA
CCCACGGCATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAG
GAGATCGTGCTGCGCTCCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGACGCTGAA
CGAGTCCGTGGAGATCAACTGCATCCGCCCCAACACAACACGCGTAAGAGCATCCACATCG
GCCCCGCGCGCCTTCTACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTGCA
ACATCAGCAAGGCCAACTGGACCAACACCCTCGAGCAGATCGTGGAGAAGCTGCGCGAGCAG
TTCGGCAACAAGACCATCATCTTCAACAGCAGCAGCGGCGGCGACCCCGAGATCGTGTT
CCACAGCTTCAACTGCGGCGGCGAGTTCTTCTACTGCAACACCAGCCAGCTGTTCAACAGCAC
CTGGAACATCACCGAGGAGGTGAACAAGACCAAGGAGAACGACACCATCATCCTGCCCTGCC
GCATCCGCCAGATCATCAACATGTGGCAGGAGGTGGGCAAGGCCATGTACGCCCCCCCCATC
CGCGGCCAGATCAAGTGACGACGAATATTACGGCCTGCTGCTGACCCGCGACGGCGGCAC
CAACAACAACCGCACCAACGACACCGAGACCTTCCGCCCCGCGGCGGCAACATGAAGGACA
ACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGCGCATCGAGCCCCTGGGCGTGGCCCCC
ACCCAGGCCAAGCGCCGCGTGGTGACGCGGAGAAGCGCGCCGTGGGCGTGGGCGCCCTGTT
CATCGGCTTCTGGGCGCCGCCGGGAGCACCATGGGCGCCGCTCCGTGACCCTGACCGTGCA
GGCCCGCCAGCTGCTGAGCGGCATCGTGACGAGCAGACAACCTGCTGCGCGCCATCGAGG
CCCAGCAGCACCTGCTGACGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCATCCTG
GCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGACGCGGCAAGCT
GATCTGCACCAACCACCGTGCCCTGGAACAGCAGCTGGAGCAACAAGAGCCTGACCGAGATCT
GGGACAACATGACCTGGATGGAGTGGGAGCGCGAGATCGGCAACTACACCGGCCTGATCTAC
AACCTGATCGAGATCGCCCAGAACAGCAGGAGAAGAAGCAGCAGGAGCTGCTGGAGCTGG
ACAAGTGGGCCAGCCTGTGGAACCTGGTTCGACATCACCAACTGGCTGTGGTACATCCGCATCT
TCATCATGATCGTGGGCGGCCTGATCGGCCTGCGCATCGTGTTCCGCGTGCTGAGCATCGTGA
ACCGCGTGCGCCAGGGCTACAGCCCCATCAGCCTGCAGACCCGCTGCCCGCCAGCGCGGC
CCCGACCGCCCCGAGGGCATCGAGGAGGAGGGCGGCGAGCGCGACCGCGACCGCAGCAACC
GCCTGGTGACGGCCTGCTGGCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTACGCT
ACCACCGCCTGCGCGACCTGCTGCTGATCGTGGCCCGCATCGTGGAGCTGCTGGGCGCCGCG
GCTGGGAGGGCCCTGAAGTACTGGTGGAACTGCTGCAGTACTGGAGCCAGGAGCTGAAGAGC
AGCGCCGTGAGCCTGTTCAACGCCACCGCCATCGCCGTGGCCGAGGGCACCGACCGCATCATC
GAGATCGTGACGCGCATCTTCCGCGCCGTGATCCACATCCCCCGCCGCATCCGCCAGGGCCTG
GAGCGCGCCCTGCTGTAAGATATCGGATCCTCTAGA

FIG. 54

(SEQ ID NO:67)

67 / 131

gp160.modUS4 del 128-194

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGGAGCA
GTCTTCGTTTTCGCCCAGCGCCACCACCGTGCTGTGGGTGACCGTGACTACGGCGTGCCCGTG
TGGAAGGAGGCCACCACCACCCTGTTCTGCGCCAGCGACGCCAAGGCTTACAAGGCCGAGGC
CCACAACGTGTGGGCCACCCACGCCTGCGTGCCACCGACCCCAACCCCAAGGAGGTGAACC
TGACCAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGAGCAGATGCATGAG
GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAAGCTGACCCCCCTGTGCGTG
GGGGCAGGGAAGTGCAGAGACCAGCGTGATACCCAGGCCTGCCCAAGGTGAGCTTCGAGCC
CATCCCCATCCACTACTGCGCCCCCGCGGCTTCGCCATCCTGAAGTGCAAGGACAAGAAGTT
CAACGGCACCCGGCCCCCTGCAAGAACGTGAGCACCGTGCAAGTGACCCACGGCATCCGCCCCG
TGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGAGATCGTGCTGCGCTCC
GAGAACTTCAACGACAACGCCAAGACCATCATCGTGACGCTGAACGAGTCCGTGGAGATCAA
CTGCATCCGCCCCAACAAACAACACGCGTAAGAGCATCCACATCGGCCCGGCGCGCCTTCTA
CGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCAAGGCCAACT
GGACCAACACCCTCGAGCAGATCGTGGAGAAGCTGCGCGAGCAGTTTCGGCAACAACAAGACC
ATCATCTTCAACAGCAGCAGCGCGCGGACCCGAGATCGTGTTCCACAGCTTCAACTGCGGC
GGCGAGTTCTTCTACTGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCACCGAGGAG
GTGAACAAGACCAAGGAGAACGACACCATCATCCTGCCCTGCCGATCCGCCAGATCATCAA
CATGTGGCAGGAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCCAGATCAAGTGCA
GCAGCAATATTACCGGCTGCTGCTGACCCGCGACGGCGGCACCAACAACAACCGCACCAAC
GACACCGAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAAGTGGCGCAGCGAGCTGTA
CAAGTACAAGGTGGTGCGCATCGAGCCCTGGGCGTGGCCCCACCCAGGCCAAGCGCCGCG
TGGTGACGCGGAGAAGCGCGCCGTGGGCGCTGGGCGCCCTGTTTCATCGGCTTCTGGGCGCCG
CCGGGAGCACCATGGGCGCCGCTCCGTGACCCTGACCGTGACGGCCCGCCAGCTGCTGAGC
GGCATCGTGACGAGCAGACAACCTGCTGCGCGCCATCGAGGCCAGCAGCACCTGCTGCA
GCTGACCGTGTTGGGCATCAAGCAGCTGCAGGCCCGCATCCTGGCCGTGGAGCGCTACCTGA
AGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCACCGTG
CCCTGGAACAGCAGCTGGAGCAACAAGAGCCTGACCGAGATCTGGGACAACATGACCTGGAT
GGAGTGGGAGCGCGAGATCGGCAACTACACCGGCTGATCTACAACCTGATCGAGATCGCCC
AGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAAGTGGGCCAGCCTGTG
GAACTGGTTTCGACATCACCAACTGGCTGTGGTACATCCGCATCTTCATCATGATCGTGGGCGG
CCTGATCGGCCTGCGCATCGTGTTGCGCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTA
CAGCCCCATCAGCCTGCAGACCCGCTGCCCGCCAGCGCGGCCCGACCGCCCCGAGGGCA
TCGAGGAGGAGGGCGGCGAGCGGACCGGACCGCAGCAACCGCCTGGTGACGGCCTGCTG
GCCCTGATCTGGGACGACCTGCGCAGCCTGTGCTGTTGCTGTTGAGCTACACCGCCTGCGCGACCTG
CTGCTGATCGTGGCCCGCATCGTGGAGCTGCTGGGCGCCGCGGCTGGGAGGCCCTGAAGTAC
TGGTGGAACTGCTGCAGTACTGGAGCCAGGAGCTGAAGAGCAGCGCCGTGAGCCTGTTCAA
CGCCACCGCATCGCCGTGGCCGAGGGCACCGACCGCATCATCGAGATCGTGACGCGCATCTT
CCGCGCCGTGATCCACATCCCCCGCGCATCCGCCAGGGCCTGGAGCGCGCCCTGCTGTAAGA
TATCGGATCCTCTAGA

FIG. 55

(SEQ ID NO:68)

68 / 131

Env_US4_C4wt

GACACTATCATACTCCCATGCAGAATAAGACAAATTATAAACATGTGGCAAGAAGTAGG
AAAAGCAATGTATGCCCCCTCCCATCAGAGGACAAATTAAATGTTTCATCAAATATTACAG
GGCTGCTATTAACTAGAGATGGTGGT

FIG. 56

(SEQ ID NO:69)

Env_SF162_C4wt

GGAACATATCACACTCCCATGCAGAATAAAACAAATTATAAACAGGTGGCAGGAAGTAGG
AAAAGCAATGTATGCCCCCTCCCATCAGAGGACAAATTAGATGCTCATCAAATATTACAG
GACTGCTATTAAACAAGAGATGGTGGT

FIG. 57

(SEQ ID NO:70)

Env_US4_C4mod

GACACCATCATCCTGCCCTGCCGCATCCGCCAGATCATCAACATGTGGCAGGAGGTGGG
CAAGGCCATGTACGCCCCCCCCCATCCGCGGCCAGATCAAGTGCAGCAGCAACATCACCG
GCCTGCTGCTGACCCGCGACGGCGGC

FIG. 58

(SEQ ID NO:71)

Env_SF162_C4mod

GGCACCATCACCTGCCCTGCCGCATCAAGCAGATCATCAACCGCTGGCAGGAGGTGGG
CAAGGCCATGTACGCCCCCCCCCATCCGCGGCCAGATCCGCTGCAGCAGCAACATCACCG
GCCTGCTGCTGACCCGCGACGGCGGC

FIG. 59

(SEQ ID NO:72)

69 / 131

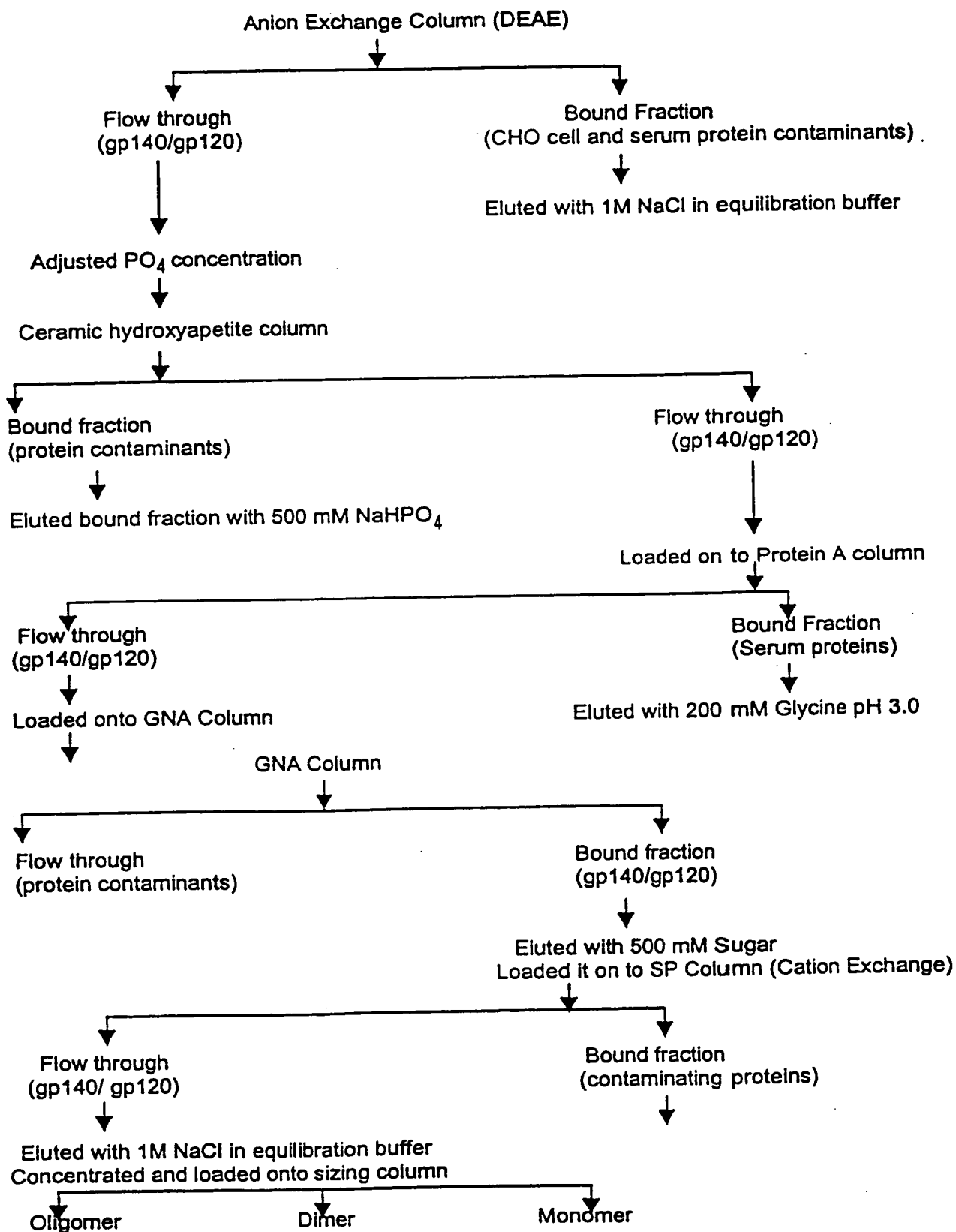


FIG. 60

70 / 131

gp160mod.us4.gag.modSF2

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGGA
GCAGTCTTCGTTTTCGCCAGCGCCACCACCGTGCTGTGGGTGACCGTGTACTIONACGGCGTG
CCCGTGTGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCTTACAAG
GCCGAGGCCCAACGTGTGGGCCACCCACGCCTGCGTGCCCAACGACCCCAACCCCCAG
GAGGTGAACCTGACCAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAG
CAGATGCATGAGGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTG
ACCCCCCTGTGCGTGACCCTGAACTGCACCGACAAGCTGACCGGCAGCACCAACGGCACC
AACAGCACCAGCGGCACCAACAGCACCAGCGGCACCAACAGCACCAGCACCAACAGCACC
GACAGCTGGGAGAAGATGCCCCGAGGGCGAGATCAAGAACTGCAGCTTCAACATCACCACC
AGCGTGCGCGACAAGGTGCAGAAGGAGTACAGCCTGTTCTACAAGCTGGACGTGGTGCCC
ATCGACAACGACAACGCCAGCTACCGCCTGATCAACTGCAACACCAGCGTGATCACCCAG
GCCTGCCCCAAGGTGAGCTTCGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTTC
GCCATCCTGAAGTGCAAGGACAAGAAGTTCAACGGCACCGGCCCTGCAAGAACGTGAGC
ACCGTGCGAGTGACCCACGGCATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGC
AGCCTGGCCGAGGAGGAGATCGTGCTGCGCTCCGAGAACTTCACCGACAACGCCAAGACC
ATCATCGTGCGAGCTGAACGAGTCCGTGGAGATCAACTGCATCCGCCCCAACAACAACAG
CGTAAGAGCATCCACATCGGCCCGGCCGCGCCTTCTACGCCACCGGCGACATCATCGGC
GACATCCGCCAGGCCCACTGCAACATCAGCAAGGCCAACTGGACCAACACCCTCGAGCAG
ATCGTGAGAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGACCATCATCTTCAACAGCAGC
AGCGGCGGCGACCCCGAGATCGTGTTCCACAGCTTCAACTGCGGCGGCGAGTTCTTCTAC
TGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCACCGAGGAGGTGAACAAGACC
AAGGAGAACGACACCATCATCCTGCCCTGCCGCATCCGCCAGATCATCAACATGTGGCAG
GAGGTGGGCAAGGCCATGTACGCCCCCCCCCATCCGCGGCCAGATCAAGTGCGAGCAGCAAT
ATTACCGGCCTGCTGCTGACCCGCGACGGCGGCACCAACAACAACCGCACCAACGACACC
GAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAACCTGGCGCAGCGAGCTGTACAAG
TACAAGGTGGTGCGCATCGAGCCCCTGGGCGTGCGCCCCACCCAGGCCAAGCGCCGCGTG
GTGCAGCGCGAGAAGCGCGCCGTGGGCCTGGGCGCCCTGTTTCATCGGCTTCTGGGCGCC
GCCGGGAGCACCATGGGCGCCGCTCCGTGACCCTGACCGTGCGAGGCCCAGCAGCACCTG
AGCGGCATCGTGCGAGCAGCAGAACAACCTGCTGCGCGCCATCGAGGCCCAGCAGCACCTG
CTGCAGCTGACCGTGTTGGGCGATCAAGCAGCTGCAGGCCCCGATCCTGGCCGTGGAGCGC
TACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACC
ACCACCGTGCCCTGGAACAGCAGCTGGAGCAACAAGAGCCTGACCGAGATCTGGGACAAC
ATGACCTGGATGGAGTGGGAGCGCGAGATCGGCAACTACACCGGCCTGATCTACAACCTG
ATCGAGATCGCCAGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAAG
TGGGCCAGCCTGTGGAACCTGGTTCGACATCACCAACTGGCTGTGGTACATCCGCATCTTC
ATCATGATCGTGGGCGGCCTGATCGGCCTGCGCATCGTGTTGCGCGTGCTGAGCATCGTG
AACCGCGTGCGCCAGGGCTACAGCCCCATCAGCCTGCAGACCCGCTGCCCCGCCAGCGC
GGCCCCGACCGCCCCGAGGGCATCGAGGAGGAGGGCGGCGAGCGCGACCGCGACCGCAGC
AACCGCCTGGTGACGGCCTGCTGGCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTG
TTCAGCTACCACCGCCTGCGCGACCTGCTGCTGATCGTGCCCCGATCGTGAGAGCTGCTG
GGCCGCCGCGGCTGGGAGGCCCTGAAGTACTGGTGAACCTGCTGCAGTACTGGAGCCAG
GAGCTGAAGAGCAGCGCCGTGAGCCTGTTCAACGCCACCGCCATCGCCGTGGCCGAGGGC
ACCGACCGCATCATCGAGATCGTGCGAGCGCATCTTCCGCGCCGTGATCCACATCCCCCGC
CGCATCCGCCAGGGCCTGGAGCGCGCCCTGCTGTAAGATATCGGATCCTCTAGAGAATTC

FIG. 61A

(SEQ ID NO:73)

SUBSTITUTE SHEET (RULE 26)

71 / 131

CGCCCCCCCCCCCCCCCCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAAGCCGC
TTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTCCACCATATTGCCGTCTTTT
GGCAATGTGAGGGCCCCGGAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGGTCTT
TCCCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTG
GAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCA
CCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCG
GCACAACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCC
TCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTTGTATGGGATCT
GATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAACGTCTA
GGCCCCCGGAACCACGGGGACGTGGTTTTCTTTGAAAAACACGATAATACCATGGGCGC
CCGCGCCAGCGTGCTGAGCGGCGGCGAGCTGGACAAGTGGGAGAAGATCCGCCTGCGCCC
CGGCGGCAAGAAGAAGTACAAGCTGAAGCACATCGTGTGGGCCAGCCGCGAGCTGGAGCG
CTTCGCCGTGAACCCCGGCCTGCTGGAGACCAGCGAGGGCTGCCGCCAGATCCTGGGCCA
GCTGCAGCCCAGCCTGCAGACCGGCAGCGAGGAGCTGCGCAGCCTGTACAACACCGTGGC
CACCTGTACTGCGTGCACCAGCGCATCGACGTCAAGGACACCAAGGAGGCCCTGGAGAA
GATCGAGGAGGAGCAGAACAAGTCCAAGAAGAAGGCCAGCAGGCCGCCGCCGCCGCCG
CACCGGCAACAGCAGCCAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCA
GATGGTGCACCAGGCCATCAGCCCCCGCACCCCTGAACGCCTGGGTGAAGGTGGTGGAGGA
GAAGGCCTTCAGCCCCGAGGTGATCCCCATGTTTCAGCGCCCTGAGCGAGGGCGCCACCCC
CCAGGACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCT
GAAGGAGACCATCAACGAGGAGGCCGCCGAGTGGGACCGCGTGCACCCCGTGCACGCCGG
CCCCATCGCCCCCGGCCAGATGCGCGAGCCCCCGCGGCAGCGACATCGCCGGCACCACCAG
CACCTGCAGGAGCAGATCGGCTGGATGACCAACAACCCCCCATCCCCGTGGGCGAGAT
CTACAAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCACCAG
CATCCTGGACATCCGCCAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTA
CAAGACCCTGCGCGCTGAGCAGGCCAGCCAGGACGTGAAGAACTGGATGACCGAGACCCT
GCTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGAAGGCTCTCGGCCCGCGGC
CACCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCCGGCCACAAGGCCCG
CGTGCTGGCCGAGGCGATGAGCCAGGTGACGAACCCGGCGACCATCATGATGCAGCGCGG
CAACTTCCGCAACCAGCGGAAGACCGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACAC
CGCCAGGAAGTGC CGCGCCCCCGCAAGAAGGGCTGCTGGCGCTGCGGCCGCGAGGGCCA
CCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCTGGGCAAGATCTGGCCCAGCTA
CAAGGGCCGCCCCGGCAACTTCTGCGAGCCGCCCCGAGCCCACCGCCCCCCCCGAGGA
GAGCTTCCGCTTCGGCGAGGAGAAGACCACCCCGAGCCAGAAGCAGGAGCCCATCGACAA
GGAGCTGTACCCCTGACCAGCCTGCGCAGCCTGTTCCGGCAACGACCCCGAGCAGCCAGTA
AGAATTCAGACTCGAGCAAGTCTAGA

FIG. 61B

(SEQ ID NO:73)

72 / 131

gp160mod.SF162.gag.modSF2

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGG
AGCAGTCTTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCG
TGCCCGTGTGGAAGGAGGCCACCACCACCCTGTTCTGCGCCAGCGACGCCAAGGCCTAC
GACACCGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCACCCGACCCCAACCC
CCAGGAGATCGTGTGCTGGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGG
TGGAGCAGATGCACGAGGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTG
AAGCTGACCCCCCTGTGCGTGACCCTGCACTGCACCAACCTGAAGAACGCCACCAACAC
CAAGAGCAGCAACTGGAAGGAGATGGACCGCGGCGAGATCAAGAACTGCAGCTTCAAGG
TGACCACCAGCATCCGCAACAAGATGCAGAAGGAGTACGCCCTGTTCTACAAGCTGGAC
GTGGTGCCCATCGACAACGACAACACCAGCTACAAGCTGATCAACTGCAACACCAGCGT
GATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCATCCCCATCCACTACTGCGCCC
CCGCCGGCTTCGCCATCCTGAAGTGCAACGACAAGAAGTTCAACGGCAGCGGCCCTGC
ACCAACGTGAGCACCGTGCAGTGCACCCACGGCATCCGCCCCGTGGTGAGCACCCAGCT
GCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGTGGTGATCCGCAGCGAGAAGTTACCG
ACAACGCCAAGACCATCATCGTGCAGCTGAAGGAGAGCGTGGAGATCAACTGCACCCGC
CCCAACAACAACACCCGCAAGAGCATCACCATCGGCCCCGGCCGCGCCTTCTACGCCAC
CGGCGACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCGAGAAGTGGA
ACAACACCCTGAAGCAGATCGTGACCAAGCTGCAGGCCAGTTTCGGCAACAAGACCATC
GTGTTCAAGCAGAGCAGCGGCGGCGACCCCGAGATCGTGATGCACAGCTTCAACTGCGG
CGGCGAGTTCTTCTACTGCAACAGCACCCAGCTGTTCAACAGCACCTGGAACAACACCA
TCGGCCCCAACAACACCAACGGCACCATCACCTGCCCTGCCGCATCAAGCAGATCATC
AACCGCTGGCAGGAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCCAGATCCG
CTGCAGCAGCAACATCACCGGCCTGCTGCTGACCCGCGACGGCGGCAAGGAGATCAGCA
ACACCACCGAGATCTTCCGCCCCGGCGGCGGCGACATGCGCGACAAGTGGCGCAGCGAG
CTGTACAAGTACAAGGTGGTGAAGATCGAGCCCCCTGGGCGTGGCCCCCAACAAGGCCAA
GCGCCGCGTGGTGCAGCGCGAGAAGCGCGCCGTGACCCTGGGCGCCATGTTCTTGGGCT
TCCTGGGCGCCCGCCGGCAGCACCATGGGCGCCCGCAGCCTGACCCTGACCGTGCAGGCC
CGCCAGCTGCTGAGCGGCATCGTGCAGCAGCAGAACAACTGCTGCGCGCCATCGAGGC
CCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGC
TGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGC
AAGCTGATCTGCACCACCGCCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGA
CCAGATCTGGAACAACATGACCTGGATGGAGTGGGAGCGCGAGATCGACAACCTACACCA
ACCTGATCTACACCCTGATCGAGGAGAGCCAGAACCAGCAGGAGAAGAACGAGCAGGAG
CTGCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAAGTGGTTCGACATCAGCAAGTGGCT
GTGGTACATCAAGATCTTCATCATGATCGTGGGCGGCCTGGTGGGCCTGCGCATCGTGT
TCACCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCCTGAGCTTCCAG
ACCCGCTTCCCCGCCCCCGCGGCCCGACCGCCCCGAGGGCATCGAGGAGGAGGGCGG
CGAGCGCGACCGCGACCGCAGCAGCCCCCTGGTGCACGGCCTGCTGGCCCTGATCTGGG
ACGACCTGCGCAGCCTGTGCCTGTTTACGCTACCACCGCCTGCGCGACCTGATCCTGATC
GCCGCCCGCATCGTGGAGCTGCTGGGCCCGCGCGGCTGGGAGGCCCTGAAGTACTGGGG
CAACCTGCTGCAGTACTGGATCCAGGAGCTGAAGAACAGCGCCGTGAGCCTGTTTCGACG
CCATCGCCATCGCCGTGGCCGAGGGCACCGACCGCATCATCGAGGTGGCCAGCGCATC
GGCCGCGCCTTCTGACATCCCCCGCCGCATCCGCCAGGGCTTCGAGCGCGCCCTGCT

FIG. 62A

(SEQ ID NO:74)

SUBSTITUTE SHEET (RULE 26)

73 / 131

GTA ACTCGAGCAAGTCTAGAGAATTCCGCCCCCCCCCCCCCCCCCTCTCCCTCCCC
CCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATAT
GTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCCGAAACCTGGCCCTG
TCTTCTTGACGAGCATTCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCTG
TTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGT
AGCGACCCTTTGCAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAA
AGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGT
TGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAA
GGATGCCCAGAAGGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCT
TTACATGTGTTTAGTCGAGGTTAAAAAACGTCTAGGCCCCCGAACCACGGGGACGTG
GTTTTCTTTGAAAAACACGATAATACCATGGGCGCCCGCGCCAGCGTGTGAGCGGCG
GCGAGCTGGACAAGTGGGAGAAGATCCGCCTGCGCCCCGCGGCAAGAAGAAGTACAAG
CTGAAGCACATCGTGTGGGCCAGCCGCGAGCTGGAGCGCTTCGCCGTGAACCCCGGCCT
GCTGGAGACCAGCGAGGGCTGCCGCCAGATCCTGGGCCAGCTGCAGCCCAGCCTGCAGA
CCGGCAGCGAGGAGCTGCGCAGCCTGTACAACACCGTGGCCACCCTGTACTGCGTGCAC
CAGCGCATCGACGTCAAGGACACCAAGGAGGCCCTGGAGAAGATCGAGGAGGAGCAGAA
CAAGTCCAAGAAGAAGGCCAGCAGGCCGCGCGCCGCGCCGCCACCGGCAACAGCAGCC
AGGTGAGCCAGA ACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTGCACCAGGCC
ATCAGCCCCCGCACCCCTGAACGCCTGGGTGAAGGTGGTGGAGGAGAAGGCCCTTCAGCCC
CGAGGTGATCCCCATGTTTCAGCGCCCTGAGCGAGGGCGCCACCCCCAGGACCTGAACA
CGATGTTGAACACCGTGGGCGGCCACCAGGCCGCGCATGCAGATGCTGAAGGAGACCATC
AACGAGGAGGCCGCGAGTGGGACCGCGTGCACCCCGTGCACGCCGCCCCATCGCCCC
CGGCCAGATGCGCGAGCCCCGCGGCAGCGACATCGCCGGCACCAACAGCACCTGCAGG
AGCAGATCGGCTGGATGACCAACAACCCCCCATCCCCGTGGGCGAGATCTACAAGCGG
TGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCACCAGCATCCTGGA
CATCCGCCAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTACAAGACCC
TGCGCGCTGAGCAGGCCAGCCAGGACGTGAAGAACTGGATGACCGAGACCCTGCTGGTG
CAGAACGCCAACCCCCGACTGCAAGACCATCCTGAAGGCTCTCGGCCCCGCGGCCACCCT
GGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCGGCCACAAGGCCGCGTGC
TGGCCGAGGCGATGAGCCAGGTGACGAACCCGGCGACCATCATGATGCAGCGCGGCAAC
TTCCGCAACCAGCGGAAGACCGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACACCGC
CAGGAAC TGCCGCGCCCCCGCAAGAAGGGCTGCTGGCGCTGCGGCCGCGAGGGCCACC
AGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCCTGGGCAAGATCTGGCCCAGCTAC
AAGGGCCGCCCCGGCAACTTCCTGCAGAGCCGCCCCGAGCCCACCGCCCCCCCCGAGGA
GAGCTTCCGCTTCGGCGAGGAGAAGACCACCCCGAGCCAGAAGCAGGAGCCCATCGACA
AGGAGCTGTACCCCTGACCAGCCTGCGCAGCCTGTTCCGGCAACGACCCCGAGCAGCCAG
TAAGAATTCAGACTCGAGCAAGTCTAGA

FIG. 62B

(SEQ ID NO:74)

74 / 131

gp160modUS4.delV1/V2.gag.modSF2

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGGA
GCAGTCTTCGTTTCGCCCAGCGCCACCACCGTGCTGTGGGTGACCGTGTAACGGCGTG
CCCGTGTGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCTTACAAG
GCCGAGGCCCAACGCTGTGGGCCACCCACGCCTGCGTGCCCAACCGACCCCAACCCCGAG
GAGGTGAACCTGACCAACGCTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAG
CAGATGCATGAGGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGCGGCCG
GGCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCATCCCCATCCACTACTGCGCCCCCGCC
GGCTTCGCCATCCTGAAGTGCAAGGACAAGAAGTTCAACGGCACCGGCCCTGCAAGAAC
GTGAGCACCGTGCAAGTGACCCACGGCATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTG
AACGGCAGCCTGGCCGAGGAGGAGATCGTGCTGCGCTCCGAGAACTTCACCGACAACGCC
AAGACCATCATCGTGAGCTGAACGAGTCCGTGGAGATCAACTGCATCCGCCCCAACAAC
AACACGCGTAAGAGCATCCACATCGGCCCCGGCGCGCCTTCTACGCCACCGGCGACATC
ATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCAAGGCCAACTGGACCAACACCCTC
GAGCAGATCGTGGAAGCTGCGCGAGCAGTTCGGCAACAACAAGACCATCATCTTCAAC
AGCAGCAGCGGCGGCGACCCCGAGATCGTGTTCCACAGCTTCAACTGCGGCGGCGAGTTC
TTCTACTGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCACCGAGGAGGTGAAC
AAGACCAAGGAGAACGACACCATCATCCTGCCCTGCCGCATCCGCCAGATCATCAACATG
TGGCAGGAGGTGGGCAAGGCCATGTACGCCCCCCCCCATCCGCGGCCAGATCAAGTGCAGC
AGCAATATTACCGGCCTGCTGCTGACCCGCGACGGCGGCACCAACAACAACCGCACCAAC
GACACCGAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAACCTGGCGCAGCGAGCTG
TACAAGTACAAGGTGGTGCGCATCGAGCCCCCTGGGCGTGCCCCCAACCGGCCAAGCGC
CGCGTGGTGAGCGCGAGAAGCGCGCCGTGGGCCTGGGCGCCCTGTTTCATCGGCTTCCTG
GGCGCCCGCGGGAGCACCATGGGCGCCGCCTCCGTGACCCTGACCGTGACGGCCCGCCAG
CTGCTGAGCGGCATCGTGAGCAGCAGAACAACCTGCTGCGCGCCATCGAGGCCCGAGCAG
CACCTGCTGAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCATCCTGGCCGTG
GAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATC
TGCACCACCACCGTGCCCTGGAACAGCAGCTGGAGCAACAAGAGCCTGACCGAGATCTGG
GACAACATGACCTGGATGGAGTGGGAGCGCGAGATCGGCAACTACACCGGCCTGATCTAC
AACCTGATCGAGATCGCCCAGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTG
GACAAGTGGGCCAGCCTGTGGAACCTGGTTCGACATCAACCAACTGGCTGTGGGTACATCCGC
ATCTTCATCATGATCGTGGGCGGCCTGATCGGCCTGCGCATCGTGTTTCGCCGTGCTGAGC
ATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCATCAGCCTGCAGACCCGCCTGCCCGCC
CAGCGCGGCCCGACCGCCCCGAGGGCATCGAGGAGGAGGGCGGCGAGCGCGACCGCGAC
CGCAGCAACCGCCTGGTGACGGCCTGCTGGCCCTGATCTGGGACGACCTGCGCAGCCTG
TGCTGTTCAGCTACCACCGCCTGCGCGACCTGCTGCTGATCGTGGCCCGCATCGTGGAG
CTGCTGGGCCCGCGCGGCTGGGAGGCCCTGAAGTACTGGTGGAACCTGCTGCAGTACTGG
AGCCAGGAGCTGAAGAGCAGCGCCGTGAGCCTGTTCAACGCCACCGCCATCGCCGTGGCC
GAGGGCACCGACCGCATCATCGAGATCGTGAGCGCATCTTCCGCGCCGTGATCCACATC
CCCCGCCGCATCCGCCAGGGCCTGGAGCGCGCCCTGCTGTAAGATATCGGATCCTCTAGA
GAATTCGCCCCCCCCCCCCCCCCCCCCCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGA
AGCCGCTTGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATATTGCCG
TCTTTTGGCAATGTGAGGGCCCCGGAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGG
GGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTT

FIG. 63A

(SEQ ID NO:75)

75 / 131

CCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAAC
CCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATAACCTGCA
AAGGCGGCACAACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGG
CTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTTGTATG
GGATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTAGTCGAGGTTAAAAAA
CGTCTAGGCCCCCGAACCACGGGGACGTGGTTTTCTTTGAAAAACACGATAATACCAT
GGGCGCCCCGCGCCAGCGTGCTGAGCGGCGGCGAGCTGGACAAGTGGGAGAAGATCCGCCT
GCGCCCCGCGCGCAAGAAGAAGTACAAGCTGAAGCACATCGTGTGGGCCAGCCGCGAGCT
GGAGCGCTTCGCCGTGAACCCCGGCCTGCTGGAGACCAGCGAGGGCTGCCGCCAGATCCT
GGGCCAGCTGCAGCCAGCCTGCAGACCGGCAGCGAGGAGCTGCGCAGCCTGTACAACAC
CGTGGCCACCCTGTACTGCGTGCAACAGCGCATCGACGTCAAGGACACCAAGGAGGCCCT
GGAGAAGATCGAGGAGGAGCAGAACAAAGTCCAAGAAGAAGGCCAGCAGGCCGCCGCCGC
CGCCGGCACCCGCAACAGCAGCCAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCA
GGGCCAGATGGTGCACCAGGCCATCAGCCCCCGCACCCCTGAACGCCTGGGTGAAGGTGGT
GGAGGAGAAGGCCTTCAGCCCCGAGGTGATCCCCATGTTTCAAGCGCCCTGAGCGAGGGCGC
CACCCCCCAGGACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCA
GATGCTGAAGGAGACCATCAACGAGGAGGCCCGCCGAGTGGGACCGCGTGCACCCCGTGCA
CGCCGGCCCCCATCGCCCCCGGCCAGATGCGCGAGCCCCGCGGCAGCGACATCGCCGGCAC
CACCAGCACCCCTGCAGGAGCAGATCGGCTGGATGACCAACAACCCCCCATCCCCGTGGG
CGAGATCTACAAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCAGGATGTACAGCCC
CACCAGCATCCTGGACATCCGCCAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCG
CTTCTACAAGACCCTGCGCGCTGAGCAGGCCAGCCAGGACGTGAAGAACTGGATGACCGA
GACCCTGCTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGAAGGCTCTCGGCCC
CGCGGCCACCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCGGCCACAA
GGCCCGCGTGCTGGCCGAGGCGATGAGCCAGGTGACGAACCCGGCGACCATCATGATGCA
GCGCGGCAACTTCCGCAACCAGCGGAAGACCGTCAAGTGCTTCAACTGCGGCAAGGAGGG
CCACACCGCCAGGAAGTGCCTGCGCCCCCGCAAGAAGGGCTGCTGGCGCTGCGGCCGCGA
GGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCCTGGGCAAGATCTGGCC
CAGCTACAAGGGCCGCCCGGCCAACTTCCTGCAGAGCCGCCCGAGCCACCGCCCCCCC
CGAGGAGAGCTTCCGCTTCGGCGAGGAGAAGACCACCCCGAGCCAGAAGCAGGAGCCCAT
CGACAAGGAGCTGTACCCCTGACCAGCCTGCGCAGCCTGTTCCGGCAACGACCCAGCAG
CCAGTAAGAATTCACTCGAGCAAGTCTAGA

FIG. 63B

(SEQ ID NO:75)

76 / 131

gp160.modSF162.delV2.gag.modSF2

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGGA
GCAGTCTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTAACGCGCTG
CCCGTGTGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCCTACGAC
ACCGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCCAACGACCCCAACCCCCAG
GAGATCGTGCTGGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAG
CAGATGCACGAGGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTG
ACCCCCCTGTGCGTGACCCTGCACTGCACCAACCTGAAGAACGCCACCAACACCAAGAGC
AGCAACTGGAAGGAGATGGACCGCGGCGAGATCAAGAACTGCAGCTTCAAGGTGGGCGCC
GGCAAGCTGATCAACTGCAACACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTTC
GAGCCCATCCCCATCCACTACTGCGCCCCCGCGGCTTCGCCATCCTGAAGTGCAACGAC
AAGAAGTTCAACGGCAGCGGCCCTGCACCAACGTGAGCACCGTGAGTGACCCACGGC
ATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGTG
GTGATCCGCAGCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGACGCTGAAGGAG
AGCGTGGAGATCAACTGCACCCGCCCAACAACAACACCCGCAAGAGCATCACCATCGGC
CCCGGCCGCGCCTTCTACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTGC
AACATCAGCGGCGAGAAGTGAACAACACCTGAAGCAGATCGTGACCAAGCTGCAGGCC
CAGTTCGGCAACAAGACCATCGTGTTCAAGCAGAGCAGCGGCGGCGACCCCGAGATCGTG
ATGCACAGCTTCAACTGCGGCGGCGAGTTCTTCTACTGCAACAGCACCCAGCTGTTCAAC
AGCACCTGGAACAACACCATCGGCCCAACAACACCAACGGCACCATCACCTGCCCTGC
CGCATCAAGCAGATCATCAACCGCTGGCAGGAGGTGGGCAAGGCCATGTACGCCCCCCCC
ATCCGCGGCCAGATCCGCTGCAGCAGCAACATCACCGCCTGCTGCTGACCCGCGACGGC
GGCAAGGAGATCAGCAACACCACCGAGATCTTCCGCCCGGCGGCGGCGACATGCGCGAC
AACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCCTGGGCGTGGCC
CCCACCAAGGCCAAGCGCCGCGTGCTGCAGCGCGAGAAGCGCGCCGTGACCCTGGGCGCC
ATGTTCTCTGGGCTTCTTGGGCGCCGCGGCGAGCACCATGGGCGCCCGCAGCCTGACCCTG
ACCGTGACGGCCCGCCAGCTGCTGAGCGGCATCGTGACGAGCAGAGAACAACCTGCTGCGC
GCCATCGAGGCCCGAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAG
GCCCCGCTGCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGC
TGCAGCGCAAGCTGATCTGCACCACCGCCGTGCCCTGGAACGCCAGCTGGAGCAACAAG
AGCCTGGACCAGATCTGGAACAACATGACCTGGATGGAGTGGGAGCGCGAGATCGACAAC
TACACCAACCTGATCTACACCCTGATCGAGGAGAGCCAGAACCAGCAGGAGAAGAACGAG
CAGGAGCTGCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAAGTGGTTCGACATCAGCAAG
TGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGGCGGCCTGGTGGGCCTGCGCATC
GTGTTACCCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCCTGAGCTTC
CAGACCCGCTTCCCCGCCCCCGCGGCCCGACCGCCCCGAGGGCATCGAGGAGGAGGGC
GGCGAGCGCGACCGCGACCGCAGCAGCCCCCTGGTGACGGCCTGCTGGCCCTGATCTGG
GACGACCTGCGCAGCCTGTGCCTGTTACGCTACCAACCGCCTGCGCGACCTGATCCTGATC
GCCGCCCGCATCGTGGAGCTGCTGGGCGCGCGGCTGGGAGGCCCTGAAGTACTGGGGC
AACCTGCTGCAGTACTGGATCCAGGAGCTGAAGAACAGCGCCGTGAGCCTGTTTCGACGCC
ATCGCCATCGCCGTGGCCGAGGGCACCGACCGCATCATCGAGGTGGCCCAGCGCATCGGC
CGCGCCTTCTGACATCCCCCGCCGCATCCGCCAGGGCTTCGAGCGCGCCCTGCTGTAA
CTCGAGCAAGTCTAGAGAATTCCGCCCCCCCCCCCCCCCCCTCTCCCTCCCCCCCCCCC
TAACGTTACTGGCCGAAGCCGCTTGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATT
TTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCCGAAACCTGGCCCTGTCTTCTT

FIG. 64A
(SEQ ID NO:76)

77 / 131

GACGAGCATTTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGT
CGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACCCT
TTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGT
ATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGT
GGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAA
GGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTA
GTCGAGGTTAAAAAACGTCTAGGCCCCCGAACCACGGGGACGTGGTTTTTCCTTTGAAA
AACACGATAATACCATGGGCGCCCGCGCCAGCGTGCTGAGCGGCGGCGAGCTGGACAAGT
GGGAGAAGATCCGCCTGCGCCCCGGCGGCAAGAAGAAGTACAAGCTGAAGCACATCGTGT
GGGCCAGCCGCGAGCTGGAGCGCTTCGCCGTGAACCCCGGCCTGCTGGAGACCAGCGAGG
GCTGCCGCCAGATCCTGGGCCAGCTGCAGCCCAGCCTGCAGACCGGCAGCGAGGAGCTGC
GCAGCCTGTACAACACCGTGGCCACCCTGTACTGCGTGCACCAGCGCATCGACGTCAAGG
ACACCAAGGAGGCCCTGGAGAAGATCGAGGAGGAGCAGAACAAGTCCAAGAAGAAGGCC
AGCAGGCCGCGCGCCGCGCCGGCACCGGCAACAGCAGCCAGGTGAGCCAGAATACTACCCCA
TCGTGCAGAACCTGCAGGGCCAGATGGTGCACCAGGCCATCAGCCCCCGCACCTGAACG
CCTGGGTGAAGGTGGTGGAGGAGAAGGCCTTCAGCCCCGAGGTGATCCCCATGTTTCAGCG
CCCTGAGCGAGGGCGCCACCCCCCAGGACCTGAACACGATGTTGAACACCGTGGGCGGCC
ACCAGGCCGCCATGCAGATGCTGAAGGAGACCATCAACGAGGAGGCCGCCGAGTGGGACC
GCGTGCACCCCGTGCACGCCGGCCCCATCGCCCCCGGCCAGATGCGCGAGCCCCGCGGCA
GCGACATCGCCGGCACCAACAGCACCTGCAGGAGCAGATCGGCTGGATGACCAACAACC
CCCCCATCCCCGTGGGCGAGATCTACAAGCGGTGGATCATCCTGGGCCTGAACAAGATCG
TGCGGATGTACAGCCCCACCAGCATCCTGGACATCCGCCAGGGCCCCAAGGAGCCCTTCC
GCGACTACGTGGACCGCTTCTACAAGACCCTGCGCGCTGAGCAGGCCAGCCAGGACGTGA
AGAACTGGATGACCGAGACCCTGCTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCC
TGAAGGCTCTCGGCCCCGCGGCCACCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGG
GCGGCCCGGCCACAAGGCCCGCGTGCTGGCCGAGGCGATGAGCCAGGTGACGAACCCGG
CGACCATCATGATGCAGCGCGGCAACTTCCGCAACCAGCGGAAGACCGTCAAGTGCTTCA
ACTGCGGCAAGGAGGGCCACACCGCCAGGAACTGCCGCGCCCCCGCAAGAAGGGCTGCT
GGCGCTGCGGCCGCGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCC
TGGGCAAGATCTGGCCCAGCTACAAGGGCCGCCCCGGCAACTTCCTGCAGAGCCGCCCCG
AGCCCACCGCCCCCCCCGAGGAGAGCTTCCGCTTCGGCGAGGAGAAGACCACCCCGAGCC
AGAAGCAGGAGCCCATCGACAAGGAGCTGTACCCCCTGACCAGCCTGCGCAGCCTGTTTCG
GCAACGACCCCAGCAGCCAGTAAGAATTCAGACTCGAGCAAGTCTAGA

FIG. 64B

(SEQ ID NO:76)

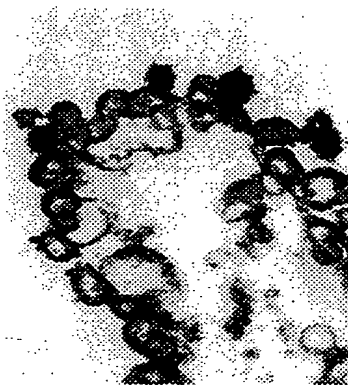
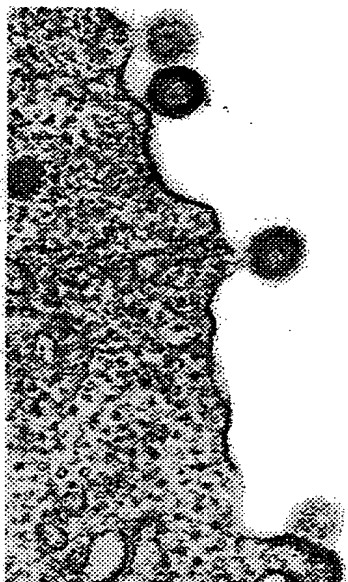


FIG. 65C

FIG. 65B

FIG. 65A

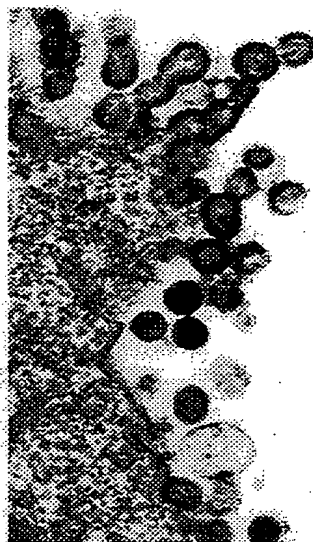


FIG. 65F

FIG. 65E

FIG. 65D

79 / 131

	1	50
gp160.modSF162	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCT
gp160.modSF162.delV2	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCT
gp160.modSF162.delV1V2	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCT
gp140.modSF162	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCT
gp140.mut.modSF162	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCT
gp140.mut7.modSF162	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCT
gp140.mut8.modSF162	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCT
gp120.modSF162	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCT
Consensus	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCT
	51	100
gp160.modSF162	(51)	GCTGTGTGGAGCAGTCTTCGTTTCGCCACGCGCCGTGGAGAGCTGTGGG
gp160.modSF162.delV2	(51)	GCTGTGTGGAGCAGTCTTCGTTTCGCCACGCGCCGTGGAGAGCTGTGGG
gp160.modSF162.delV1V2	(51)	GCTGTGTGGAGCAGTCTTCGTTTCGCCACGCGCCGTGGAGAGCTGTGGG
gp140.modSF162	(51)	GCTGTGTGGAGCAGTCTTCGTTTCGCCACGCGCCGTGGAGAGCTGTGGG
gp140.mut.modSF162	(51)	GCTGTGTGGAGCAGTCTTCGTTTCGCCACGCGCCGTGGAGAGCTGTGGG
gp140.mut7.modSF162	(51)	GCTGTGTGGAGCAGTCTTCGTTTCGCCACGCGCCGTGGAGAGCTGTGGG
gp140.mut8.modSF162	(51)	GCTGTGTGGAGCAGTCTTCGTTTCGCCACGCGCCGTGGAGAGCTGTGGG
gp120.modSF162	(51)	GCTGTGTGGAGCAGTCTTCGTTTCGCCACGCGCCGTGGAGAGCTGTGGG
Consensus	(51)	GCTGTGTGGAGCAGTCTTCGTTTCGCCACGCGCCGTGGAGAGCTGTGGG
	101	150
gp160.modSF162	(101)	TGACCGTGTAACGGCGTGCCCGTGTGGAAGGAGGCCACCAACCCCTG
gp160.modSF162.delV2	(101)	TGACCGTGTAACGGCGTGCCCGTGTGGAAGGAGGCCACCAACCCCTG
gp160.modSF162.delV1V2	(101)	TGACCGTGTAACGGCGTGCCCGTGTGGAAGGAGGCCACCAACCCCTG
gp140.modSF162	(101)	TGACCGTGTAACGGCGTGCCCGTGTGGAAGGAGGCCACCAACCCCTG
gp140.mut.modSF162	(101)	TGACCGTGTAACGGCGTGCCCGTGTGGAAGGAGGCCACCAACCCCTG
gp140.mut7.modSF162	(101)	TGACCGTGTAACGGCGTGCCCGTGTGGAAGGAGGCCACCAACCCCTG
gp140.mut8.modSF162	(101)	TGACCGTGTAACGGCGTGCCCGTGTGGAAGGAGGCCACCAACCCCTG
gp120.modSF162	(101)	TGACCGTGTAACGGCGTGCCCGTGTGGAAGGAGGCCACCAACCCCTG
Consensus	(101)	TGACCGTGTAACGGCGTGCCCGTGTGGAAGGAGGCCACCAACCCCTG

FIG. 66A-1

80 / 131

gp160.modSF162	(151)	TTCTGCGCCAGCGACGCCAAGCCTACGACACCGAGGTGCACAACGTTGTG	200
gp160.modSF162.delV2	(151)	TTCTGCGCCAGCGACGCCAAGCCTACGACACCGAGGTGCACAACGTTGTG	
gp160.modSF162.delV1V2	(151)	TTCTGCGCCAGCGACGCCAAGCCTACGACACCGAGGTGCACAACGTTGTG	
gp140.modSF162	(151)	TTCTGCGCCAGCGACGCCAAGCCTACGACACCGAGGTGCACAACGTTGTG	
gp140.mut.modSF162	(151)	TTCTGCGCCAGCGACGCCAAGCCTACGACACCGAGGTGCACAACGTTGTG	
gp140.mut7.modSF162	(151)	TTCTGCGCCAGCGACGCCAAGCCTACGACACCGAGGTGCACAACGTTGTG	
gp140.mut8.modSF162	(151)	TTCTGCGCCAGCGACGCCAAGCCTACGACACCGAGGTGCACAACGTTGTG	
gp120.modSF162	(151)	TTCTGCGCCAGCGACGCCAAGCCTACGACACCGAGGTGCACAACGTTGTG	
Consensus	(151)	TTCTGCGCCAGCGACGCCAAGCCTACGACACCGAGGTGCACAACGTTGTG	250
gp160.modSF162	(201)	GGCCACCCACGCCCTGCGTGCCCAACCGACCCCAACCCCCAGGAGATCGTGC	
gp160.modSF162.delV2	(201)	GGCCACCCACGCCCTGCGTGCCCAACCGACCCCAACCCCCAGGAGATCGTGC	
gp160.modSF162.delV1V2	(201)	GGCCACCCACGCCCTGCGTGCCCAACCGACCCCAACCCCCAGGAGATCGTGC	
gp140.modSF162	(201)	GGCCACCCACGCCCTGCGTGCCCAACCGACCCCAACCCCCAGGAGATCGTGC	
gp140.mut.modSF162	(201)	GGCCACCCACGCCCTGCGTGCCCAACCGACCCCAACCCCCAGGAGATCGTGC	
gp140.mut7.modSF162	(201)	GGCCACCCACGCCCTGCGTGCCCAACCGACCCCAACCCCCAGGAGATCGTGC	
gp140.mut8.modSF162	(201)	GGCCACCCACGCCCTGCGTGCCCAACCGACCCCAACCCCCAGGAGATCGTGC	
gp120.modSF162	(201)	GGCCACCCACGCCCTGCGTGCCCAACCGACCCCAACCCCCAGGAGATCGTGC	
Consensus	(201)	GGCCACCCACGCCCTGCGTGCCCAACCGACCCCAACCCCCAGGAGATCGTGC	300
gp160.modSF162	(251)	TGGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAG	
gp160.modSF162.delV2	(251)	TGGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAG	
gp160.modSF162.delV1V2	(251)	TGGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAG	
gp140.modSF162	(251)	TGGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAG	
gp140.mut.modSF162	(251)	TGGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAG	
gp140.mut7.modSF162	(251)	TGGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAG	
gp140.mut8.modSF162	(251)	TGGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAG	

FIG. 66A-2

81 / 131

gp120.modSF162	(251)	TGGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACACATGGTGGAG	350
Consensus	(251)	TGGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACACATGGTGGAG	350
gp160.modSF162	(301)	CAGATGCACGAGGACATCATCAGCCTGTGGACCAGAGCCTGAAGCCCTG	301
gp160.modSF162.delV2	(301)	CAGATGCACGAGGACATCATCAGCCTGTGGACCAGAGCCTGAAGCCCTG	301
gp160.modSF162.delV1V2	(301)	CAGATGCACGAGGACATCATCAGCCTGTGGACCAGAGCCTGAAGCCCTG	301
gp140.modSF162	(301)	CAGATGCACGAGGACATCATCAGCCTGTGGACCAGAGCCTGAAGCCCTG	301
gp140.mut.modSF162	(301)	CAGATGCACGAGGACATCATCAGCCTGTGGACCAGAGCCTGAAGCCCTG	301
gp140.mut7.modSF162	(301)	CAGATGCACGAGGACATCATCAGCCTGTGGACCAGAGCCTGAAGCCCTG	301
gp140.mut8.modSF162	(301)	CAGATGCACGAGGACATCATCAGCCTGTGGACCAGAGCCTGAAGCCCTG	301
gp120.modSF162	(301)	CAGATGCACGAGGACATCATCAGCCTGTGGACCAGAGCCTGAAGCCCTG	301
Consensus	(301)	CAGATGCACGAGGACATCATCAGCCTGTGGACCAGAGCCTGAAGCCCTG	301
gp160.modSF162	(351)	CGTGAAGCTGACCCCTGTGCGTGACCCCTGCACTGCACCAACCTGAAGA	400
gp160.modSF162.delV2	(351)	CGTGAAGCTGACCCCTGTGCGTGACCCCTGCACTGCACCAACCTGAAGA	400
gp160.modSF162.delV1V2	(351)	CGTGAAGCTGACCCCTGTGCGTGACCCCTGCACTGCACCAACCTGAAGA	400
gp140.modSF162	(351)	CGTGAAGCTGACCCCTGTGCGTGACCCCTGCACTGCACCAACCTGAAGA	400
gp140.mut.modSF162	(351)	CGTGAAGCTGACCCCTGTGCGTGACCCCTGCACTGCACCAACCTGAAGA	400
gp140.mut7.modSF162	(351)	CGTGAAGCTGACCCCTGTGCGTGACCCCTGCACTGCACCAACCTGAAGA	400
gp140.mut8.modSF162	(351)	CGTGAAGCTGACCCCTGTGCGTGACCCCTGCACTGCACCAACCTGAAGA	400
gp120.modSF162	(351)	CGTGAAGCTGACCCCTGTGCGTGACCCCTGCACTGCACCAACCTGAAGA	400
Consensus	(351)	CGTGAAGCTGACCCCTGTGCGTGACCCCTGCACTGCACCAACCTGAAGA	400
gp160.modSF162	(401)	ACGCCACCAACACCAAGAGCAGCAACTGGAAGGAGATGGACCGCGCGGAG	450
gp160.modSF162.delV2	(401)	ACGCCACCAACACCAAGAGCAGCAACTGGAAGGAGATGGACCGCGCGGAG	450
gp160.modSF162.delV1V2	(375)	-----	450
gp140.modSF162	(401)	ACGCCACCAACACCAAGAGCAGCAACTGGAAGGAGATGGACCGCGCGGAG	450
gp140.mut.modSF162	(401)	ACGCCACCAACACCAAGAGCAGCAACTGGAAGGAGATGGACCGCGCGGAG	450
gp140.mut7.modSF162	(401)	ACGCCACCAACACCAAGAGCAGCAACTGGAAGGAGATGGACCGCGCGGAG	450
gp140.mut8.modSF162	(401)	ACGCCACCAACACCAAGAGCAGCAACTGGAAGGAGATGGACCGCGCGGAG	450
gp120.modSF162	(401)	ACGCCACCAACACCAAGAGCAGCAACTGGAAGGAGATGGACCGCGCGGAG	450
Consensus	(401)	ACGCCACCAACACCAAGAGCAGCAACTGGAAGGAGATGGACCGCGCGGAG	450

FIG. 66A-3

82 / 131

gp160.modSF162	(451)	ATCAAGAACTGCAGCTTCAAGGTGACCAACCAAGCATCCGGCAACAAGATGCA	500
gp160.modSF162.delV2	(451)	ATCAAGAACTGCAGCTTCAAGGTGGC-----	
gp160.modSF162.delV1V2	(376)	-----GGC-----	
gp140.modSF162	(451)	ATCAAGAACTGCAGCTTCAAGGTGACCAACCAAGCATCCGGCAACAAGATGCA	
gp140.mut.modSF162	(451)	ATCAAGAACTGCAGCTTCAAGGTGACCAACCAAGCATCCGGCAACAAGATGCA	
gp140.mut7.modSF162	(451)	ATCAAGAACTGCAGCTTCAAGGTGACCAACCAAGCATCCGGCAACAAGATGCA	
gp140.mut8.modSF162	(451)	ATCAAGAACTGCAGCTTCAAGGTGACCAACCAAGCATCCGGCAACAAGATGCA	
gp120.modSF162	(451)	ATCAAGAACTGCAGCTTCAAGGTGACCAACCAAGCATCCGGCAACAAGATGCA	
Consensus	501	ATCAAGAACTGCAGCTTCAAGGTGACCAACCAAGCATCCGGCAACAAGATGCA	550
gp160.modSF162	(501)	GAAGGAGTACGCCCTGTTCTACAAGCTGGACGTGGTGTGCCCCATCGACAACG	
gp160.modSF162.delV2	(478)	-----GCC-----GG-----	
gp160.modSF162.delV1V2	(379)	-----GCC-----GG-----	
gp140.modSF162	(501)	GAAGGAGTACGCCCTGTTCTACAAGCTGGACGTGGTGTGCCCCATCGACAACG	
gp140.mut.modSF162	(501)	GAAGGAGTACGCCCTGTTCTACAAGCTGGACGTGGTGTGCCCCATCGACAACG	
gp140.mut7.modSF162	(501)	GAAGGAGTACGCCCTGTTCTACAAGCTGGACGTGGTGTGCCCCATCGACAACG	
gp140.mut8.modSF162	(501)	GAAGGAGTACGCCCTGTTCTACAAGCTGGACGTGGTGTGCCCCATCGACAACG	
gp120.modSF162	(501)	GAAGGAGTACGCCCTGTTCTACAAGCTGGACGTGGTGTGCCCCATCGACAACG	
Consensus	551	GAAGGAGTACGCCCTGTTCTACAAGCTGGACGTGGTGTGCCCCATCGACAACG	600
gp160.modSF162	(551)	ACAACACCAGCTACAAGCTGATCAACTGCAACACCAGCGTGATCACCAG	
gp160.modSF162.delV2	(492)	-----CAAGCTGATCAACTGCAACACCAGCGTGATCACCAG	
gp160.modSF162.delV1V2	(384)	-----CAACTGCCAGACCAGCGTGATCACCAG	
gp140.modSF162	(551)	ACAACACCAGCTACAAGCTGATCAACTGCAACACCAGCGTGATCACCAG	
gp140.mut.modSF162	(551)	ACAACACCAGCTACAAGCTGATCAACTGCAACACCAGCGTGATCACCAG	

FIG. 66A-4

83 / 131

gp140.mut7.modSF162	(551)	ACAACACCAGCTACAAGCTGATCAACTGCAACACACAGCGTGATCACCAG	650
gp140.mut8.modSF162	(551)	ACAACACCAGCTACAAGCTGATCAACTGCAACACACAGCGTGATCACCAG	
gp120.modSF162	(551)	ACAACACCAGCTACAAGCTGATCAACTGCAACACACAGCGTGATCACCAG	
Consensus	(551)	ACAACACCAGCTACAAGCTGATCAACTGCAACACACAGCGTGATCACCAG	650
gp160.modSF162	(601)	GCCTGCCCCAAGGTGAGCTTCGAGGCCCATCCCCATCCACTACTGCGCCCC	601
gp160.modSF162.delV2	(520)	GCCTGCCCCAAGGTGAGCTTCGAGGCCCATCCCCATCCACTACTGCGCCCC	
gp160.modSF162.delV1V2	(412)	GCCTGCCCCAAGGTGAGCTTCGAGGCCCATCCCCATCCACTACTGCGCCCC	
gp140.modSF162	(601)	GCCTGCCCCAAGGTGAGCTTCGAGGCCCATCCCCATCCACTACTGCGCCCC	
gp140.mut.modSF162	(601)	GCCTGCCCCAAGGTGAGCTTCGAGGCCCATCCCCATCCACTACTGCGCCCC	
gp140.mut7.modSF162	(601)	GCCTGCCCCAAGGTGAGCTTCGAGGCCCATCCCCATCCACTACTGCGCCCC	
gp140.mut8.modSF162	(601)	GCCTGCCCCAAGGTGAGCTTCGAGGCCCATCCCCATCCACTACTGCGCCCC	
gp120.modSF162	(601)	GCCTGCCCCAAGGTGAGCTTCGAGGCCCATCCCCATCCACTACTGCGCCCC	
Consensus	(601)	GCCTGCCCCAAGGTGAGCTTCGAGGCCCATCCCCATCCACTACTGCGCCCC	700
gp160.modSF162	(651)	CGCCGGCTTCGCCATCCTGAAGTGCAACGACAAAGAAAGTTCAACGGCAGCG	651
gp160.modSF162.delV2	(570)	CGCCGGCTTCGCCATCCTGAAGTGCAACGACAAAGAAAGTTCAACGGCAGCG	
gp160.modSF162.delV1V2	(462)	CGCCGGCTTCGCCATCCTGAAGTGCAACGACAAAGAAAGTTCAACGGCAGCG	
gp140.modSF162	(651)	CGCCGGCTTCGCCATCCTGAAGTGCAACGACAAAGAAAGTTCAACGGCAGCG	
gp140.mut.modSF162	(651)	CGCCGGCTTCGCCATCCTGAAGTGCAACGACAAAGAAAGTTCAACGGCAGCG	
gp140.mut7.modSF162	(651)	CGCCGGCTTCGCCATCCTGAAGTGCAACGACAAAGAAAGTTCAACGGCAGCG	
gp140.mut8.modSF162	(651)	CGCCGGCTTCGCCATCCTGAAGTGCAACGACAAAGAAAGTTCAACGGCAGCG	
gp120.modSF162	(651)	CGCCGGCTTCGCCATCCTGAAGTGCAACGACAAAGAAAGTTCAACGGCAGCG	
Consensus	(651)	CGCCGGCTTCGCCATCCTGAAGTGCAACGACAAAGAAAGTTCAACGGCAGCG	750
gp160.modSF162	(701)	GCCCTGCACCAACGTGAGCACCGTGCAAGTGCAACCCACGGCATCCGCCCC	701
gp160.modSF162.delV2	(620)	GCCCTGCACCAACGTGAGCACCGTGCAAGTGCAACCCACGGCATCCGCCCC	
gp160.modSF162.delV1V2	(512)	GCCCTGCACCAACGTGAGCACCGTGCAAGTGCAACCCACGGCATCCGCCCC	
gp140.modSF162	(701)	GCCCTGCACCAACGTGAGCACCGTGCAAGTGCAACCCACGGCATCCGCCCC	
gp140.mut.modSF162	(701)	GCCCTGCACCAACGTGAGCACCGTGCAAGTGCAACCCACGGCATCCGCCCC	
gp140.mut7.modSF162	(701)	GCCCTGCACCAACGTGAGCACCGTGCAAGTGCAACCCACGGCATCCGCCCC	
gp140.mut8.modSF162	(701)	GCCCTGCACCAACGTGAGCACCGTGCAAGTGCAACCCACGGCATCCGCCCC	
gp120.modSF162	(701)	GCCCTGCACCAACGTGAGCACCGTGCAAGTGCAACCCACGGCATCCGCCCC	
Consensus	(701)	GCCCTGCACCAACGTGAGCACCGTGCAAGTGCAACCCACGGCATCCGCCCC	

FIG. 66A-5

gp160.modSF162	(751)	GTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGT	751
gp160.modSF162.delV2	(670)	GTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGT	800
gp160.modSF162.delV1V2	(562)	GTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGT	
gp140.modSF162	(751)	GTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGT	
gp140.mut.modSF162	(751)	GTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGT	
gp140.mut7.modSF162	(751)	GTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGT	
gp140.mut8.modSF162	(751)	GTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGT	
gp120.modSF162	(751)	GTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGT	
Consensus	(751)	GTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGT	850
gp160.modSF162	(801)	GGTGATCCGACGCGAGAACTTCACCGACAAACGCCAAGACCATCATCTGTGC	801
gp160.modSF162.delV2	(720)	GGTGATCCGACGCGAGAACTTCACCGACAAACGCCAAGACCATCATCTGTGC	
gp160.modSF162.delV1V2	(612)	GGTGATCCGACGCGAGAACTTCACCGACAAACGCCAAGACCATCATCTGTGC	
gp140.modSF162	(801)	GGTGATCCGACGCGAGAACTTCACCGACAAACGCCAAGACCATCATCTGTGC	
gp140.mut.modSF162	(801)	GGTGATCCGACGCGAGAACTTCACCGACAAACGCCAAGACCATCATCTGTGC	
gp140.mut7.modSF162	(801)	GGTGATCCGACGCGAGAACTTCACCGACAAACGCCAAGACCATCATCTGTGC	
gp140.mut8.modSF162	(801)	GGTGATCCGACGCGAGAACTTCACCGACAAACGCCAAGACCATCATCTGTGC	
gp120.modSF162	(801)	GGTGATCCGACGCGAGAACTTCACCGACAAACGCCAAGACCATCATCTGTGC	
Consensus	(801)	GGTGATCCGACGCGAGAACTTCACCGACAAACGCCAAGACCATCATCTGTGC	900
gp160.modSF162	(851)	AGCTGAAGGAGAGCGTGGAGATCAACTGCACCCCGCCCCCAACAACACACC	851
gp160.modSF162.delV2	(770)	AGCTGAAGGAGAGCGTGGAGATCAACTGCACCCCGCCCCCAACAACACACC	
gp160.modSF162.delV1V2	(662)	AGCTGAAGGAGAGCGTGGAGATCAACTGCACCCCGCCCCCAACAACACACC	

FIG. 66A-6

85 / 131

gp140.modSF162	(851)	AGCTGAAGGAGAGCGTGGAGATCAACTGCACCCGCCCCCAACAACAACACC
gp140.mut.modSF162	(851)	AGCTGAAGGAGAGCGTGGAGATCAACTGCACCCGCCCCCAACAACAACACC
gp140.mut7.modSF162	(851)	AGCTGAAGGAGAGCGTGGAGATCAACTGCACCCGCCCCCAACAACAACACC
gp140.mut8.modSF162	(851)	AGCTGAAGGAGAGCGTGGAGATCAACTGCACCCGCCCCCAACAACAACACC
gp120.modSF162	(851)	AGCTGAAGGAGAGCGTGGAGATCAACTGCACCCGCCCCCAACAACAACACC
Consensus	901	AGCTGAAGGAGAGCGTGGAGATCAACTGCACCCGCCCCCAACAACAACACC
gp160.modSF162	(901)	CGCAAGAGCATCACCATCGGCCCGGGCGCGCCCTTCTACGCCACCGGCGGA
gp160.modSF162.delV2	(820)	CGCAAGAGCATCACCATCGGCCCGGGCGCGCCCTTCTACGCCACCGGCGGA
gp160.modSF162.delV1V2	(712)	CGCAAGAGCATCACCATCGGCCCGGGCGCGCCCTTCTACGCCACCGGCGGA
gp140.modSF162	(901)	CGCAAGAGCATCACCATCGGCCCGGGCGCGCCCTTCTACGCCACCGGCGGA
gp140.mut.modSF162	(901)	CGCAAGAGCATCACCATCGGCCCGGGCGCGCCCTTCTACGCCACCGGCGGA
gp140.mut7.modSF162	(901)	CGCAAGAGCATCACCATCGGCCCGGGCGCGCCCTTCTACGCCACCGGCGGA
gp140.mut8.modSF162	(901)	CGCAAGAGCATCACCATCGGCCCGGGCGCGCCCTTCTACGCCACCGGCGGA
gp120.modSF162	(901)	CGCAAGAGCATCACCATCGGCCCGGGCGCGCCCTTCTACGCCACCGGCGGA
Consensus	951	CGCAAGAGCATCACCATCGGCCCGGGCGCGCCCTTCTACGCCACCGGCGGA
gp160.modSF162	(951)	CATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCGGAGAAGT
gp160.modSF162.delV2	(870)	CATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCGGAGAAGT
gp160.modSF162.delV1V2	(762)	CATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCGGAGAAGT
gp140.modSF162	(951)	CATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCGGAGAAGT
gp140.mut.modSF162	(951)	CATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCGGAGAAGT
gp140.mut7.modSF162	(951)	CATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCGGAGAAGT
gp140.mut8.modSF162	(951)	CATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCGGAGAAGT
gp120.modSF162	(951)	CATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCGGAGAAGT
Consensus	1000	CATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCGGAGAAGT

FIG. 66A-7

gp160.modSF162	1001	GGAACAACACCCCTGAAGCAGATCGTGACCAAGCTGCAGGCCAGTTCGGC	1050
gp160.modSF162.delV2	(1001)	GGAACAACACCCCTGAAGCAGATCGTGACCAAGCTGCAGGCCAGTTCGGC	
gp160.modSF162.delV1V2	(920)	GGAACAACACCCCTGAAGCAGATCGTGACCAAGCTGCAGGCCAGTTCGGC	
gp140.modSF162	(812)	GGAACAACACCCCTGAAGCAGATCGTGACCAAGCTGCAGGCCAGTTCGGC	
gp140.modSF162	(1001)	GGAACAACACCCCTGAAGCAGATCGTGACCAAGCTGCAGGCCAGTTCGGC	
gp140.modSF162	(1001)	GGAACAACACCCCTGAAGCAGATCGTGACCAAGCTGCAGGCCAGTTCGGC	
gp140.mut.modSF162	(1001)	GGAACAACACCCCTGAAGCAGATCGTGACCAAGCTGCAGGCCAGTTCGGC	
gp140.mut7.modSF162	(1001)	GGAACAACACCCCTGAAGCAGATCGTGACCAAGCTGCAGGCCAGTTCGGC	
gp140.mut8.modSF162	(1001)	GGAACAACACCCCTGAAGCAGATCGTGACCAAGCTGCAGGCCAGTTCGGC	
gp120.modSF162	(1001)	GGAACAACACCCCTGAAGCAGATCGTGACCAAGCTGCAGGCCAGTTCGGC	
Consensus	(1001)	GGAACAACACCCCTGAAGCAGATCGTGACCAAGCTGCAGGCCAGTTCGGC	1100
gp160.modSF162	1051	ACAAGACCATCGTGTTCAGCAGACGAGCGGGCGGACCCCGAGATCGT	
gp160.modSF162.delV2	(1051)	ACAAGACCATCGTGTTCAGCAGACGAGCGGGCGGACCCCGAGATCGT	
gp160.modSF162.delV1V2	(970)	ACAAGACCATCGTGTTCAGCAGACGAGCGGGCGGACCCCGAGATCGT	
gp140.modSF162	(862)	AACAAGACCATCGTGTTCAGCAGACGAGCGGGCGGACCCCGAGATCGT	
gp140.modSF162	(1051)	AACAAGACCATCGTGTTCAGCAGACGAGCGGGCGGACCCCGAGATCGT	
gp140.mut.modSF162	(1051)	AACAAGACCATCGTGTTCAGCAGACGAGCGGGCGGACCCCGAGATCGT	
gp140.mut7.modSF162	(1051)	AACAAGACCATCGTGTTCAGCAGACGAGCGGGCGGACCCCGAGATCGT	
gp140.mut8.modSF162	(1051)	AACAAGACCATCGTGTTCAGCAGACGAGCGGGCGGACCCCGAGATCGT	
gp120.modSF162	(1051)	AACAAGACCATCGTGTTCAGCAGACGAGCGGGCGGACCCCGAGATCGT	
Consensus	(1051)	AACAAGACCATCGTGTTCAGCAGACGAGCGGGCGGACCCCGAGATCGT	1150
gp160.modSF162	1101	GATGCACAGCTTCAACTGCGGGCGGAGTTCTTCTACTGCAACAGCACCC	
gp160.modSF162.delV2	(1101)	GATGCACAGCTTCAACTGCGGGCGGAGTTCTTCTACTGCAACAGCACCC	
gp160.modSF162.delV1V2	(1020)	GATGCACAGCTTCAACTGCGGGCGGAGTTCTTCTACTGCAACAGCACCC	
gp140.modSF162	(912)	GATGCACAGCTTCAACTGCGGGCGGAGTTCTTCTACTGCAACAGCACCC	
gp140.modSF162	(1101)	GATGCACAGCTTCAACTGCGGGCGGAGTTCTTCTACTGCAACAGCACCC	
gp140.mut.modSF162	(1101)	GATGCACAGCTTCAACTGCGGGCGGAGTTCTTCTACTGCAACAGCACCC	
gp140.mut7.modSF162	(1101)	GATGCACAGCTTCAACTGCGGGCGGAGTTCTTCTACTGCAACAGCACCC	
gp140.mut8.modSF162	(1101)	GATGCACAGCTTCAACTGCGGGCGGAGTTCTTCTACTGCAACAGCACCC	
gp120.modSF162	(1101)	GATGCACAGCTTCAACTGCGGGCGGAGTTCTTCTACTGCAACAGCACCC	
Consensus	(1101)	GATGCACAGCTTCAACTGCGGGCGGAGTTCTTCTACTGCAACAGCACCC	1200
gp160.modSF162	1151	AGCTGTTCAACAGCACCTTGGAACAACACCATCGGGCCCCCAACAACCAAC	
	(1151)	AGCTGTTCAACAGCACCTTGGAACAACACCATCGGGCCCCCAACAACCAAC	

FIG. 66A-8

87 / 131

gp160.modSF162.delV2	(1070)	AGCTGTTCAACAGCACCTGGAAACAACACCATCGGGCCCCAACACACCAAC	1250
gp160.modSF162.delV1V2	(962)	AGCTGTTCAACAGCACCTGGAAACAACACCATCGGGCCCCAACACACCAAC	
gp140.modSF162	(1151)	AGCTGTTCAACAGCACCTGGAAACAACACCATCGGGCCCCAACACACCAAC	
gp140.mut.modSF162	(1151)	AGCTGTTCAACAGCACCTGGAAACAACACCATCGGGCCCCAACACACCAAC	
gp140.mut7.modSF162	(1151)	AGCTGTTCAACAGCACCTGGAAACAACACCATCGGGCCCCAACACACCAAC	
gp140.mut8.modSF162	(1151)	AGCTGTTCAACAGCACCTGGAAACAACACCATCGGGCCCCAACACACCAAC	
gp120.modSF162	(1151)	AGCTGTTCAACAGCACCTGGAAACAACACCATCGGGCCCCAACACACCAAC	
Consensus	(1151)	AGCTGTTCAACAGCACCTGGAAACAACACCATCGGGCCCCAACACACCAAC	1251
gp160.modSF162	(1201)	GGCACCATCACCCCTGCCCTGCCGCATCAAGCAGATCATCAACCGCTGGCA	
gp160.modSF162.delV2	(1120)	GGCACCATCACCCCTGCCCTGCCGCATCAAGCAGATCATCAACCGCTGGCA	
gp160.modSF162.delV1V2	(1012)	GGCACCATCACCCCTGCCCTGCCGCATCAAGCAGATCATCAACCGCTGGCA	
gp140.modSF162	(1201)	GGCACCATCACCCCTGCCCTGCCGCATCAAGCAGATCATCAACCGCTGGCA	
gp140.mut.modSF162	(1201)	GGCACCATCACCCCTGCCCTGCCGCATCAAGCAGATCATCAACCGCTGGCA	
gp140.mut7.modSF162	(1201)	GGCACCATCACCCCTGCCCTGCCGCATCAAGCAGATCATCAACCGCTGGCA	
gp140.mut8.modSF162	(1201)	GGCACCATCACCCCTGCCCTGCCGCATCAAGCAGATCATCAACCGCTGGCA	
gp120.modSF162	(1201)	GGCACCATCACCCCTGCCCTGCCGCATCAAGCAGATCATCAACCGCTGGCA	
Consensus	(1201)	GGCACCATCACCCCTGCCCTGCCGCATCAAGCAGATCATCAACCGCTGGCA	1300
gp160.modSF162	(1251)	GGAGTGGGCAAGGCCATGTACGCCCCCCCCCATCCGGGGCCAGATCCGCT	
gp160.modSF162.delV2	(1170)	GGAGTGGGCAAGGCCATGTACGCCCCCCCCCATCCGGGGCCAGATCCGCT	
gp160.modSF162.delV1V2	(1062)	GGAGTGGGCAAGGCCATGTACGCCCCCCCCCATCCGGGGCCAGATCCGCT	
gp140.modSF162	(1251)	GGAGTGGGCAAGGCCATGTACGCCCCCCCCCATCCGGGGCCAGATCCGCT	
gp140.mut.modSF162	(1251)	GGAGTGGGCAAGGCCATGTACGCCCCCCCCCATCCGGGGCCAGATCCGCT	
gp140.mut7.modSF162	(1251)	GGAGTGGGCAAGGCCATGTACGCCCCCCCCCATCCGGGGCCAGATCCGCT	
gp140.mut8.modSF162	(1251)	GGAGTGGGCAAGGCCATGTACGCCCCCCCCCATCCGGGGCCAGATCCGCT	
gp120.modSF162	(1251)	GGAGTGGGCAAGGCCATGTACGCCCCCCCCCATCCGGGGCCAGATCCGCT	
Consensus	(1251)	GGAGTGGGCAAGGCCATGTACGCCCCCCCCCATCCGGGGCCAGATCCGCT	

FIG. 66A-9

gp160.modSF162	(1301)	GCAGCAGCAACATCACCGGCCTGCTGCTGACCCCGGCGGCAAGGAG	1350
gp160.modSF162.delV2	(1220)	GCAGCAGCAACATCACCGGCCTGCTGCTGACCCCGGCGGCAAGGAG	
gp160.modSF162.delV1V2	(1112)	GCAGCAGCAACATCACCGGCCTGCTGCTGACCCCGGCGGCAAGGAG	
gp140.modSF162	(1301)	GCAGCAGCAACATCACCGGCCTGCTGCTGACCCCGGCGGCAAGGAG	
gp140.mut.modSF162	(1301)	GCAGCAGCAACATCACCGGCCTGCTGCTGACCCCGGCGGCAAGGAG	
gp140.mut7.modSF162	(1301)	GCAGCAGCAACATCACCGGCCTGCTGCTGACCCCGGCGGCAAGGAG	
gp140.mut8.modSF162	(1301)	GCAGCAGCAACATCACCGGCCTGCTGCTGACCCCGGCGGCAAGGAG	
gp120.modSF162	(1301)	GCAGCAGCAACATCACCGGCCTGCTGCTGACCCCGGCGGCAAGGAG	
Consensus	(1301)	GCAGCAGCAACATCACCGGCCTGCTGCTGACCCCGGCGGCAAGGAG	1400
gp160.modSF162	(1351)	ATCAGCAACACCAACCGAGATCTTCCGCCCCGGCGGCGACATGCGCGA	1351
gp160.modSF162.delV2	(1270)	ATCAGCAACACCAACCGAGATCTTCCGCCCCGGCGGCGACATGCGCGA	
gp160.modSF162.delV1V2	(1162)	ATCAGCAACACCAACCGAGATCTTCCGCCCCGGCGGCGACATGCGCGA	
gp140.modSF162	(1351)	ATCAGCAACACCAACCGAGATCTTCCGCCCCGGCGGCGACATGCGCGA	
gp140.mut.modSF162	(1351)	ATCAGCAACACCAACCGAGATCTTCCGCCCCGGCGGCGACATGCGCGA	
gp140.mut7.modSF162	(1351)	ATCAGCAACACCAACCGAGATCTTCCGCCCCGGCGGCGACATGCGCGA	
gp140.mut8.modSF162	(1351)	ATCAGCAACACCAACCGAGATCTTCCGCCCCGGCGGCGACATGCGCGA	
gp120.modSF162	(1351)	ATCAGCAACACCAACCGAGATCTTCCGCCCCGGCGGCGACATGCGCGA	
Consensus	(1351)	ATCAGCAACACCAACCGAGATCTTCCGCCCCGGCGGCGACATGCGCGA	1450
gp160.modSF162	(1401)	CAACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCC	
gp160.modSF162.delV2	(1320)	CAACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCC	
gp160.modSF162.delV1V2	(1212)	CAACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCC	
gp140.modSF162	(1401)	CAACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCC	
gp140.mut.modSF162	(1401)	CAACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCC	
gp140.mut7.modSF162	(1401)	CAACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCC	
gp140.mut8.modSF162	(1401)	CAACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCC	
gp120.modSF162	(1401)	CAACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCC	
Consensus	(1401)	CAACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCC	

FIG. 66A--10

89 / 131

gp160.modSF162	(1451)	TGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTGGTGACGCGCGAGAAG	1500
gp160.modSF162.delV2	(1370)	TGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTGGTGACGCGCGAGAAG	
gp160.modSF162.delV1V2	(1262)	TGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTGGTGACGCGCGAGAAG	
gp140.modSF162	(1451)	TGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTGGTGACGCGCGAGAAG	
gp140.mut.modSF162	(1451)	TGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTGGTGACGCGCGAGAAG	
gp140.mut7.modSF162	(1451)	TGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTGGTGACGCGCGAGAAG	
gp140.mut8.modSF162	(1451)	TGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTGGTGACGCGCGAGAAG	
gp120.modSF162	(1451)	TGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTGGTGACGCGCGAGAAG	
Consensus	(1451)	TGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTGGTGACGCGCGAGAAG	1550
gp160.modSF162	(1501)	CGCGCCGTGACCCCTGGGCGCCCATGTTCTGGGCTTCCTGGGCGCGCCGG	
gp160.modSF162.delV2	(1420)	CGCGCCGTGACCCCTGGGCGCCCATGTTCTGGGCTTCCTGGGCGCGCCGG	
gp160.modSF162.delV1V2	(1312)	CGCGCCGTGACCCCTGGGCGCCCATGTTCTGGGCTTCCTGGGCGCGCCGG	
gp140.modSF162	(1501)	CGCGCCGTGACCCCTGGGCGCCCATGTTCTGGGCTTCCTGGGCGCGCCGG	
gp140.mut.modSF162	(1501)	AGCGCCGTGACCCCTGGGCGCCCATGTTCTGGGCTTCCTGGGCGCGCCGG	
gp140.mut7.modSF162	(1501)	AGCGCCGTGACCCCTGGGCGCCCATGTTCTGGGCTTCCTGGGCGCGCCGG	
gp140.mut8.modSF162	(1501)	AGCGCCGTGACCCCTGGGCGCCCATGTTCTGGGCTTCCTGGGCGCGCCGG	
gp120.modSF162	(1501)	CGC-----TAACTCGAG-----	
Consensus	(1501)	CGCGCCGTGACCCCTGGGCGCCCATGTTCTGGGCTTCCTGGGCGCGCCGG	1600
gp160.modSF162	(1551)	CAGCACCATGGGCGCCCGCAGCCTGACCCCTGACCGTGACGGCCGCCAGC	
gp160.modSF162.delV2	(1470)	CAGCACCATGGGCGCCCGCAGCCTGACCCCTGACCGTGACGGCCGCCAGC	
gp160.modSF162.delV1V2	(1362)	CAGCACCATGGGCGCCCGCAGCCTGACCCCTGACCGTGACGGCCGCCAGC	
gp140.modSF162	(1551)	CAGCACCATGGGCGCCCGCAGCCTGACCCCTGACCGTGACGGCCGCCAGC	
gp140.mut.modSF162	(1551)	CAGCACCATGGGCGCCCGCAGCCTGACCCCTGACCGTGACGGCCGCCAGC	
gp140.mut7.modSF162	(1551)	CAGCACCATGGGCGCCCGCAGCCTGACCCCTGACCGTGACGGCCGCCAGC	
gp140.mut8.modSF162	(1551)	CAGCACCATGGGCGCCCGCAGCCTGACCCCTGACCGTGACGGCCGCCAGC	
gp120.modSF162	(1513)	-----	
Consensus	(1551)	CAGCACCATGGGCGCCCGCAGCCTGACCCCTGACCGTGACGGCCGCCAGC	

FIG. 66A-11

90 / 131

gp160.modSF162	(1601)	1601	TGCTGAGCGGCATCGTGCAGCAGCAGCAACAACCTGTCTGCGGCCATCGAG	1650
gp160.modSF162.delV2	(1520)		TGCTGAGCGGCATCGTGCAGCAGCAGCAACAACCTGTCTGCGGCCATCGAG	
gp160.modSF162.delV1V2	(1412)		TGCTGAGCGGCATCGTGCAGCAGCAGCAACAACCTGTCTGCGGCCATCGAG	
gp140.modSF162	(1601)		TGCTGAGCGGCATCGTGCAGCAGCAGCAACAACCTGTCTGCGGCCATCGAG	
gp140.mut.modSF162	(1601)		TGCTGAGCGGCATCGTGCAGCAGCAGCAACAACCTGTCTGCGGCCATCGAG	
gp140.mut7.modSF162	(1601)		TGCTGAGCGGCATCGTGCAGCAGCAGCAACAACCTGTCTGCGGCCATCGAG	
gp140.mut8.modSF162	(1601)		TGCTGAGCGGCATCGTGCAGCAGCAGCAACAACCTGTCTGCGGCCATCGAG	
gp120.modSF162	(1513)		-----	
Consensus	(1601)		TGCTGAGCGGCATCGTGCAGCAGCAGCAACAACCTGTCTGCGGCCATCGAG	1700
gp160.modSF162	(1651)		1651	
gp160.modSF162.delV2	(1651)		GCCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCA	
gp160.modSF162.delV1V2	(1570)		GCCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCA	
gp140.modSF162	(1462)		GCCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCA	
gp140.modSF162	(1651)		GCCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCA	
gp140.mut.modSF162	(1651)		GCCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCA	
gp140.mut7.modSF162	(1651)		GCCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCA	
gp140.mut8.modSF162	(1651)		GCCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCA	
gp120.modSF162	(1513)		-----	
Consensus	(1651)		GCCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCA	1750
gp160.modSF162	(1701)		1701	
gp160.modSF162.delV2	(1620)		GGCCCGCGTGTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGG	
gp160.modSF162.delV1V2	(1512)		GGCCCGCGTGTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGG	
gp140.modSF162	(1701)		GGCCCGCGTGTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGG	
gp140.mut.modSF162	(1701)		GGCCCGCGTGTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGG	
gp140.mut7.modSF162	(1701)		GGCCCGCGTGTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGG	
gp140.mut8.modSF162	(1701)		GGCCCGCGTGTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGG	

FIG. 66A-12

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(1513) -----
(1701) GCGCCGCGTGCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGG
1751 1800
(1751) GCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGG
(1670) GCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGG
(1562) GCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGG
(1751) GCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGG
(1751) GCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGG
(1751) GCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGG
(1751) GCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGG
(1513) -----
(1751) GCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGG
1801 1850
(1801) AACGCCAGCTGGAGCAACAAGAGCCCTGGACCAGATCTGGAACAACATGAC
(1720) AACGCCAGCTGGAGCAACAAGAGCCCTGGACCAGATCTGGAACAACATGAC
(1612) AACGCCAGCTGGAGCAACAAGAGCCCTGGACCAGATCTGGAACAACATGAC
(1801) AACGCCAGCTGGAGCAACAAGAGCCCTGGACCAGATCTGGAACAACATGAC
(1801) AACGCCAGCTGGAGCAACAAGAGCCCTGGACCAGATCTGGAACAACATGAC
(1801) AACGCCAGCTGGAGCAACAAGAGCCCTGGACCAGATCTGGAACAACATGAC
(1801) AACGCCAGCTGGAGCAACAAGAGCCCTGGACCAGATCTGGAACAACATGAC
(1513) -----
(1801) AACGCCAGCTGGAGCAACAAGAGCCCTGGACCAGATCTGGAACAACATGAC
1851 1900
(1851) CTGGATGGAGTGGGAGCGCGAGATCGACAACCTACACCAACCTGATCTACA
(1770) CTGGATGGAGTGGGAGCGCGAGATCGACAACCTACACCAACCTGATCTACA
(1662) CTGGATGGAGTGGGAGCGCGAGATCGACAACCTACACCAACCTGATCTACA
(1851) CTGGATGGAGTGGGAGCGCGAGATCGACAACCTACACCAACCTGATCTACA
(1851) CTGGATGGAGTGGGAGCGCGAGATCGACAACCTACACCAACCTGATCTACA
(1851) CTGGATGGAGTGGGAGCGCGAGATCGACAACCTACACCAACCTGATCTACA
(1851) CTGGATGGAGTGGGAGCGCGAGATCGACAACCTACACCAACCTGATCTACA
(1513) -----
(1851) CTGGATGGAGTGGGAGCGCGAGATCGACAACCTACACCAACCTGATCTACA
Consensus
gp120.modSF162
Consensus
gp160.modSF162
gp160.modSF162.delV2
gp160.modSF162.delV1V2
gp140.modSF162
gp140.mut.modSF162
gp140.mut7.modSF162
gp140.mut8.modSF162
gp120.modSF162
Consensus
gp160.modSF162
gp160.modSF162.delV2
gp160.modSF162.delV1V2
gp140.modSF162
gp140.mut.modSF162
gp140.mut7.modSF162
gp140.mut8.modSF162
gp120.modSF162
Consensus
gp160.modSF162
gp160.modSF162.delV2
gp160.modSF162.delV1V2
gp140.modSF162
gp140.mut.modSF162
gp140.mut7.modSF162
gp140.mut8.modSF162
gp120.modSF162
Consensus

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FIG. 66A-13

92 / 131

			1950
			1901
gp160.modSF162	(1901)	CCCTGATCGAGGAGAGCCAGAACACGAGGAGAGAAACGAGCAGGAGCTG	
gp160.modSF162.delV2	(1820)	CCCTGATCGAGGAGAGCCAGAACACGAGGAGAGAAACGAGCAGGAGCTG	
gp160.modSF162.delV1V2	(1712)	CCCTGATCGAGGAGAGCCAGAACACGAGGAGAGAAACGAGCAGGAGCTG	
gp140.modSF162	(1901)	CCCTGATCGAGGAGAGCCAGAACACGAGGAGAGAAACGAGCAGGAGCTG	
gp140.mut.modSF162	(1901)	CCCTGATCGAGGAGAGCCAGAACACGAGGAGAGAAACGAGCAGGAGCTG	
gp140.mut7.modSF162	(1901)	CCCTGATCGAGGAGAGCCAGAACACGAGGAGAGAAACGAGCAGGAGCTG	
gp140.mut8.modSF162	(1901)	CCCTGATCGAGGAGAGCCAGAACACGAGGAGAGAAACGAGCAGGAGCTG	
gp120.modSF162	(1513)	-----	
Consensus	(1901)	CCCTGATCGAGGAGAGCCAGAACACGAGGAGAGAAACGAGCAGGAGCTG	
			2000
			1951
gp160.modSF162	(1951)	CTGGAGCTGGACAAGTGGGCCAGCCCTGTGGAACCTGGTTCGACATCAGCAA	
gp160.modSF162.delV2	(1870)	CTGGAGCTGGACAAGTGGGCCAGCCCTGTGGAACCTGGTTCGACATCAGCAA	
gp160.modSF162.delV1V2	(1762)	CTGGAGCTGGACAAGTGGGCCAGCCCTGTGGAACCTGGTTCGACATCAGCAA	
gp140.modSF162	(1951)	CTGGAGCTGGACAAGTGGGCCAGCCCTGTGGAACCTGGTTCGACATCAGCAA	
gp140.mut.modSF162	(1951)	CTGGAGCTGGACAAGTGGGCCAGCCCTGTGGAACCTGGTTCGACATCAGCAA	
gp140.mut7.modSF162	(1951)	CTGGAGCTGGACAAGTGGGCCAGCCCTGTGGAACCTGGTTCGACATCAGCAA	
gp140.mut8.modSF162	(1951)	CTGGAGCTGGACAAGTGGGCCAGCCCTGTGGAACCTGGTTCGACATCAGCAA	
gp120.modSF162	(1513)	-----	
Consensus	(1951)	CTGGAGCTGGACAAGTGGGCCAGCCCTGTGGAACCTGGTTCGACATCAGCAA	
			2050
gp160.modSF162	(2001)	GTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGGGCGGCTGGTGG	
gp160.modSF162.delV2	(1920)	GTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGGGCGGCTGGTGG	
gp160.modSF162.delV1V2	(1812)	GTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGGGCGGCTGGTGG	
gp140.modSF162	(2001)	GTGGCTGTGGTACATCTAACTCGAG-----	
gp140.mut.modSF162	(2001)	GTGGCTGTGGTACATCTAACTCGAG-----	

FIG. 66A-14

93 / 131

gp140.mut7.modSF162	(2001)	GTGGCTGTGGTACATCTAACTCGAG-----	2100
gp140.mut8.modSF162	(2001)	GTGGCTGTGGTACATCTAACTCGAG-----	
gp120.modSF162	(1513)	-----	
Consensus	(2001)	GTGGCTGTGGTACATCTAACTCGAG	2051
gp160.modSF162	(2051)	GCCTGGGCATCGTGTTCACCGTGCTGAGCATCGTGAACCGCGTGCGCCAG	
gp160.modSF162.delV2	(1970)	GCCTGGGCATCGTGTTCACCGTGCTGAGCATCGTGAACCGCGTGCGCCAG	
gp160.modSF162.delV1V2	(1862)	GCCTGGGCATCGTGTTCACCGTGCTGAGCATCGTGAACCGCGTGCGCCAG	
gp140.modSF162	(2026)	-----	
gp140.mut.modSF162	(2026)	-----	
gp140.mut7.modSF162	(2026)	-----	
gp140.mut8.modSF162	(2026)	-----	
gp120.modSF162	(1513)	-----	
Consensus	(2051)	-----	2101
gp160.modSF162	(2101)	GGCTACAGCCCCCTGAGCTTCCAGACCCGCTTCCCCGCCCCCGGGCCCC	2150
gp160.modSF162.delV2	(2020)	GGCTACAGCCCCCTGAGCTTCCAGACCCGCTTCCCCGCCCCCGGGCCCC	
gp160.modSF162.delV1V2	(1912)	GGCTACAGCCCCCTGAGCTTCCAGACCCGCTTCCCCGCCCCCGGGCCCC	
gp140.modSF162	(2026)	-----	
gp140.mut.modSF162	(2026)	-----	
gp140.mut7.modSF162	(2026)	-----	
gp140.mut8.modSF162	(2026)	-----	
gp120.modSF162	(1513)	-----	
Consensus	(2101)	-----	2151
gp160.modSF162	(2151)	CGACCGCCCCGAGGGCATCGAGGAGGAGGGCGGCGAGCGCGACCGCGACC	2200
gp160.modSF162.delV2	(2070)	CGACCGCCCCGAGGGCATCGAGGAGGAGGGCGGCGAGCGCGACCGCGACC	
gp160.modSF162.delV1V2	(1962)	CGACCGCCCCGAGGGCATCGAGGAGGAGGGCGGCGAGCGCGACCGCGACC	
gp140.modSF162	(2026)	-----	
gp140.mut.modSF162	(2026)	-----	
gp140.mut7.modSF162	(2026)	-----	
gp140.mut8.modSF162	(2026)	-----	
gp120.modSF162	(1513)	-----	
Consensus	(2151)	-----	

FIG. 66A-15

94 / 131

2201	2250
gcagagccccctggtgcacggcctgctggcccctgatctggacgacctg	
gcagagccccctggtgcacggcctgctggcccctgatctggacgacctg	
gcagagccccctggtgcacggcctgctggcccctgatctggacgacctg	

2251	2300
gcagacctgtgccctgttcagctaccacggcctgcccgcacctgatcctgat	
gcagacctgtgccctgttcagctaccacggcctgcccgcacctgatcctgat	
gcagacctgtgccctgttcagctaccacggcctgcccgcacctgatcctgat	

2301	2350
cgccgccccgcatacgtggagctgctggcccgcccgccgctggaggccccctga	
cgccgccccgcatacgtggagctgctggcccgcccgccgctggaggccccctga	
cgccgccccgcatacgtggagctgctggcccgcccgccgctggaggccccctga	

FIG. 66A-16

95 / 131

gp140.modSF162	(2026)	-----	
gp140.mut.modSF162	(2026)	-----	
gp140.mut7.modSF162	(2026)	-----	
gp140.mut8.modSF162	(2026)	-----	
gp120.modSF162	(1513)	-----	
Consensus	(2301)	-----	
2351			
gp160.modSF162	(2351)	AGTACTGGGGCAACCTGCTGCAGTACTGGATCCAGGAGCTGAAGAACAGC	2400
gp160.modSF162.delV2	(2270)	AGTACTGGGGCAACCTGCTGCAGTACTGGATCCAGGAGCTGAAGAACAGC	
gp160.modSF162.delV1V2	(2162)	AGTACTGGGGCAACCTGCTGCAGTACTGGATCCAGGAGCTGAAGAACAGC	
gp140.modSF162	(2026)	-----	
gp140.mut.modSF162	(2026)	-----	
gp140.mut7.modSF162	(2026)	-----	
gp140.mut8.modSF162	(2026)	-----	
gp120.modSF162	(1513)	-----	
Consensus	(2351)	-----	
2401			
gp160.modSF162	(2401)	GCCGTGAGCCCTGTTTCGACGCCCATCGCCCATCGCCGTGGCCGAGGGCACCCGA	2450
gp160.modSF162.delV2	(2320)	GCCGTGAGCCCTGTTTCGACGCCCATCGCCCATCGCCGTGGCCGAGGGCACCCGA	
gp160.modSF162.delV1V2	(2212)	GCCGTGAGCCCTGTTTCGACGCCCATCGCCCATCGCCGTGGCCGAGGGCACCCGA	
gp140.modSF162	(2026)	-----	
gp140.mut.modSF162	(2026)	-----	
gp140.mut7.modSF162	(2026)	-----	
gp140.mut8.modSF162	(2026)	-----	
gp120.modSF162	(1513)	-----	
Consensus	(2401)	-----	

FIG. 66A-17

96 / 131

	2451	2500
gp160.modSF162	(2451)	CCGCATCATCGAGGTGGCCAGCGCATCGGCCGCGCCTTCCCTGCACATCC
gp160.modSF162.delV2	(2370)	CCGCATCATCGAGGTGGCCAGCGCATCGGCCGCGCCTTCCCTGCACATCC
gp160.modSF162.delV1V2	(2262)	CCGCATCATCGAGGTGGCCAGCGCATCGGCCGCGCCTTCCCTGCACATCC
gp140.modSF162	(2026)	-----
gp140.mut.modSF162	(2026)	-----
gp140.mut7.modSF162	(2026)	-----
gp140.mut8.modSF162	(2026)	-----
gp120.modSF162	(1513)	-----
Consensus	(2451)	-----
	2501	2547
gp160.modSF162	(2501)	CCCGCCGCATCCGCCAGGGCTTCGAGCGCGCCCTGCTGTAAC TCGAG
gp160.modSF162.delV2	(2420)	CCCGCCGCATCCGCCAGGGCTTCGAGCGCGCCCTGCTGTAAC TCGAG
gp160.modSF162.delV1V2	(2312)	CCCGCCGCATCCGCCAGGGCTTCGAGCGCGCCCTGCTGTAAC TCGAG
gp140.modSF162	(2026)	-----
gp140.mut.modSF162	(2026)	-----
gp140.mut7.modSF162	(2026)	-----
gp140.mut8.modSF162	(2026)	-----
gp120.modSF162	(1513)	-----
Consensus	(2501)	-----

FIG. 66A-18

97 / 131

		Start of tPA	
		1	40
gp160	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGGCTCTGCT	
gp160 del V1	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGGCTCTGCT	
gp160 del V2	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGGCTCTGCT	
gp160 del V1-2	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGGCTCTGCT	
gp 160 del 128-194	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGGCTCTGCT	
gp140TM	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGGCTCTGCT	
gp140	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGGCTCTGCT	
gp140mut	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGGCTCTGCT	
gp120	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGGCTCTGCT	
Consensus	(1)	GAATTCGCCACCATGGATGCAATGAAGAGAGGGGCTCTGCT	
		41	80
gp160	(41)	GTGTGCTGCTGCTGTGTGGAGCAGTCTTCGTTTCGCCCCAG	
gp160 del V1	(41)	GTGTGCTGCTGCTGTGTGGAGCAGTCTTCGTTTCGCCCCAG	
gp160 del V2	(41)	GTGTGCTGCTGCTGTGTGGAGCAGTCTTCGTTTCGCCCCAG	
gp160 del V1-2	(41)	GTGTGCTGCTGCTGTGTGGAGCAGTCTTCGTTTCGCCCCAG	
gp 160 del 128-194	(41)	GTGTGCTGCTGCTGTGTGGAGCAGTCTTCGTTTCGCCCCAG	
gp140TM	(41)	GTGTGCTGCTGCTGTGTGGAGCAGTCTTCGTTTCGCCCCAG	
gp140	(41)	GTGTGCTGCTGCTGTGTGGAGCAGTCTTCGTTTCGCCCCAG	
gp140mut	(41)	GTGTGCTGCTGCTGTGTGGAGCAGTCTTCGTTTCGCCCCAG	
gp120	(41)	GTGTGCTGCTGCTGTGTGGAGCAGTCTTCGTTTCGCCCCAG	
Consensus	(41)	GTGTGCTGCTGCTGTGTGGAGCAGTCTTCGTTTCGCCCCAG	
end of tPA		81	120
gp160	(81)	CGCCACCACCGTGCTGTGGGTGACCGTGTAACGCGTG	
gp160 del V1	(81)	CGCCACCACCGTGCTGTGGGTGACCGTGTAACGCGTG	
gp160 del V2	(81)	CGCCACCACCGTGCTGTGGGTGACCGTGTAACGCGTG	
gp160 del V1-2	(81)	CGCCACCACCGTGCTGTGGGTGACCGTGTAACGCGTG	
gp 160 del 128-194	(81)	CGCCACCACCGTGCTGTGGGTGACCGTGTAACGCGTG	
gp140TM	(81)	CGCCACCACCGTGCTGTGGGTGACCGTGTAACGCGTG	
gp140	(81)	CGCCACCACCGTGCTGTGGGTGACCGTGTAACGCGTG	
gp140mut	(81)	CGCCACCACCGTGCTGTGGGTGACCGTGTAACGCGTG	
gp120	(81)	CGCCACCACCGTGCTGTGGGTGACCGTGTAACGCGTG	
Consensus	(81)	CGCCACCACCGTGCTGTGGGTGACCGTGTAACGCGTG	
		121	160
gp 160	(121)	CCCGTGTGGAAGGAGGCCACCACCACCCTGTTCTGCGCCA	
gp160 del V1	(121)	CCCGTGTGGAAGGAGGCCACCACCACCCTGTTCTGCGCCA	
gp160 del V2	(121)	CCCGTGTGGAAGGAGGCCACCACCACCCTGTTCTGCGCCA	
gp160 del V1-2	(121)	CCCGTGTGGAAGGAGGCCACCACCACCCTGTTCTGCGCCA	
gp 160 del 128-194	(121)	CCCGTGTGGAAGGAGGCCACCACCACCCTGTTCTGCGCCA	
gp140TM	(121)	CCCGTGTGGAAGGAGGCCACCACCACCCTGTTCTGCGCCA	
gp140	(121)	CCCGTGTGGAAGGAGGCCACCACCACCCTGTTCTGCGCCA	
gp140mut	(121)	CCCGTGTGGAAGGAGGCCACCACCACCCTGTTCTGCGCCA	
gp120	(121)	CCCGTGTGGAAGGAGGCCACCACCACCCTGTTCTGCGCCA	
Consensus	(121)	CCCGTGTGGAAGGAGGCCACCACCACCCTGTTCTGCGCCA	

FIG. 66B-1

		98 / 131	200
		161	
gp160	(161)	GCGACGCCAAGGCTTACAAGGCCGAGGCCCAACCGTGTG	
gp160 del V1	(161)	GCGACGCCAAGGCTTACAAGGCCGAGGCCCAACCGTGTG	
gp160 del V2	(161)	GCGACGCCAAGGCTTACAAGGCCGAGGCCCAACCGTGTG	
gp160 del V1-2	(161)	GCGACGCCAAGGCTTACAAGGCCGAGGCCCAACCGTGTG	
gp 160 del 128-194	(161)	GCGACGCCAAGGCTTACAAGGCCGAGGCCCAACCGTGTG	
gp140TM	(161)	GCGACGCCAAGGCTTACAAGGCCGAGGCCCAACCGTGTG	
gp140	(161)	GCGACGCCAAGGCTTACAAGGCCGAGGCCCAACCGTGTG	
gp140mut	(161)	GCGACGCCAAGGCTTACAAGGCCGAGGCCCAACCGTGTG	
gp120	(161)	GCGACGCCAAGGCTTACAAGGCCGAGGCCCAACCGTGTG	
Consensus	(161)	GCGACGCCAAGGCTTACAAGGCCGAGGCCCAACCGTGTG	
		201	240
gp160	(201)	GGCCACCCACGCCTGCGTGCCACCGACCCCCAACCCCCAG	
gp160 del V1	(201)	GGCCACCCACGCCTGCGTGCCACCGACCCCCAACCCCCAG	
gp160 del V2	(201)	GGCCACCCACGCCTGCGTGCCACCGACCCCCAACCCCCAG	
gp160 del V1-2	(201)	GGCCACCCACGCCTGCGTGCCACCGACCCCCAACCCCCAG	
gp 160 del 128-194	(201)	GGCCACCCACGCCTGCGTGCCACCGACCCCCAACCCCCAG	
gp140TM	(201)	GGCCACCCACGCCTGCGTGCCACCGACCCCCAACCCCCAG	
gp140	(201)	GGCCACCCACGCCTGCGTGCCACCGACCCCCAACCCCCAG	
gp140mut	(201)	GGCCACCCACGCCTGCGTGCCACCGACCCCCAACCCCCAG	
gp120	(201)	GGCCACCCACGCCTGCGTGCCACCGACCCCCAACCCCCAG	
Consensus	(201)	GGCCACCCACGCCTGCGTGCCACCGACCCCCAACCCCCAG	
		241	280
gp160	(241)	GAGGTGAACCTGACCAACGTGACCGAGAACTTCAACATGT	
gp160 del V1	(241)	GAGGTGAACCTGACCAACGTGACCGAGAACTTCAACATGT	
gp160 del V2	(241)	GAGGTGAACCTGACCAACGTGACCGAGAACTTCAACATGT	
gp160 del V1-2	(241)	GAGGTGAACCTGACCAACGTGACCGAGAACTTCAACATGT	
gp 160 del 128-194	(241)	GAGGTGAACCTGACCAACGTGACCGAGAACTTCAACATGT	
gp140TM	(241)	GAGGTGAACCTGACCAACGTGACCGAGAACTTCAACATGT	
gp140	(241)	GAGGTGAACCTGACCAACGTGACCGAGAACTTCAACATGT	
gp140mut	(241)	GAGGTGAACCTGACCAACGTGACCGAGAACTTCAACATGT	
gp120	(241)	GAGGTGAACCTGACCAACGTGACCGAGAACTTCAACATGT	
Consensus	(241)	GAGGTGAACCTGACCAACGTGACCGAGAACTTCAACATGT	
		281	320
gp160	(281)	GGAAGAACAACATGGTGGAGCAGATGCATGAGGACATCAT	
gp160 del V1	(281)	GGAAGAACAACATGGTGGAGCAGATGCATGAGGACATCAT	
gp160 del V2	(281)	GGAAGAACAACATGGTGGAGCAGATGCATGAGGACATCAT	
gp160 del V1-2	(281)	GGAAGAACAACATGGTGGAGCAGATGCATGAGGACATCAT	
gp 160 del 128-194	(281)	GGAAGAACAACATGGTGGAGCAGATGCATGAGGACATCAT	
gp140TM	(281)	GGAAGAACAACATGGTGGAGCAGATGCATGAGGACATCAT	
gp140	(281)	GGAAGAACAACATGGTGGAGCAGATGCATGAGGACATCAT	
gp140mut	(281)	GGAAGAACAACATGGTGGAGCAGATGCATGAGGACATCAT	
gp120	(281)	GGAAGAACAACATGGTGGAGCAGATGCATGAGGACATCAT	
Consensus	(281)	GGAAGAACAACATGGTGGAGCAGATGCATGAGGACATCAT	
		321	360
gp160	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTG	
gp160 del V1	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTG	
gp160 del V2	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTG	
gp160 del V1-2	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGGGCGCC	
gp 160 del 128-194	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTG	
gp140TM	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTG	
gp140	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTG	
gp140mut	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTG	
gp120	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTG	
Consensus	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTG	

FIG. 66B-2

99/131		361	400
gp160	(361)	ACCCCCCTGTGCGTGACCCTGAACTGCACCGACAAGCTGA	
gp160 del V1	(361)	ACCCCCCTGTGCGTGACCCTGAACTGCACCGACAAGCTGG	
gp160 del V2	(361)	ACCCCCCTGTGCGTGACCCTGAACTGCACCGACAAGCTGA	
gp160 del V1-2	(361)	GGC-----	
gp 160 del 128-194	(361)	ACCCCCCTGTGCGTGCGGGCAGGG-----	
gp140TM	(361)	ACCCCCCTGTGCGTGACCCTGAACTGCACCGACAAGCTGA	
gp140	(361)	ACCCCCCTGTGCGTGACCCTGAACTGCACCGACAAGCTGA	
gp140mut	(361)	ACCCCCCTGTGCGTGACCCTGAACTGCACCGACAAGCTGA	
gp120	(361)	ACCCCCCTGTGCGTGACCCTGAACTGCACCGACAAGCTGA	
Consensus	(361)	ACCCCCCTGTGCGTGACCCTGAACTGCACCGACAAGCTGA	440
		401	440
gp160	(401)	CCGGCAGCACCAACGGCACCAACAGCACCAGCGGCACCAA	
gp160 del V1	(401)	GCGCCGGC-----	
gp160 del V2	(401)	CCGGCAGCACCAACGGCACCAACAGCACCAGCGGCACCAA	
gp160 del V1-2	(364)	-----	
gp 160 del 128-194	(385)	-----	
gp140TM	(401)	CCGGCAGCACCAACGGCACCAACAGCACCAGCGGCACCAA	
gp140	(401)	CCGGCAGCACCAACGGCACCAACAGCACCAGCGGCACCAA	
gp140mut	(401)	CCGGCAGCACCAACGGCACCAACAGCACCAGCGGCACCAA	
gp120	(401)	CCGGCAGCACCAACGGCACCAACAGCACCAGCGGCACCAA	
Consensus	(401)	CCGGCAGCACCAACGGCACCAACAGCACCAGCGGCACCAA	480
		441	480
gp160	(441)	CAGCACCAGCGGCACCAACAGCACCAGCACCACCAACAGCACC	
gp160 del V1	(409)	-----	
gp160 del V2	(441)	CAGCACCAGCGGCACCAACAGCACCAGCACCACCAACAGCACC	
gp160 del V1-2	(364)	-----	
gp 160 del 128-194	(385)	-----	
gp140TM	(441)	CAGCACCAGCGGCACCAACAGCACCAGCACCACCAACAGCACC	
gp140	(441)	CAGCACCAGCGGCACCAACAGCACCAGCACCACCAACAGCACC	
gp140mut	(441)	CAGCACCAGCGGCACCAACAGCACCAGCACCACCAACAGCACC	
gp120	(441)	CAGCACCAGCGGCACCAACAGCACCAGCACCACCAACAGCACC	
Consensus	(441)	CAGCACCAGCGGCACCAACAGCACCAGCACCACCAACAGCACC	520
		481	520
gp160	(481)	GACAGCTGGGAGAAGATGCCCCGAGGGCGAGATCAAGAACT	
gp160 del V1	(409)	-----GGCGAGATCAAGAACT	
gp160 del V2	(481)	GACAGCTGGGAGAAGATGCCCCGAGGGCGAGATCAAGAACT	
gp160 del V1-2	(364)	-----	
gp 160 del 128-194	(385)	-----	
gp140TM	(481)	GACAGCTGGGAGAAGATGCCCCGAGGGCGAGATCAAGAACT	
gp140	(481)	GACAGCTGGGAGAAGATGCCCCGAGGGCGAGATCAAGAACT	
gp140mut	(481)	GACAGCTGGGAGAAGATGCCCCGAGGGCGAGATCAAGAACT	
gp120	(481)	GACAGCTGGGAGAAGATGCCCCGAGGGCGAGATCAAGAACT	
Consensus	(481)	GACAGCTGGGAGAAGATGCCCCGAGGGCGAGATCAAGAACT	560
		521	560
gp160	(521)	GCAGCTTCAACATCACCACCAGCGTGCGCGACAAGGTGCA	
gp160 del V1	(521)	GCAGCTTCAACATCACCACCAGCGTGCGCGACAAGGTGCA	
gp160 del V2	(521)	GCAGCTTCAACATCGGGCGCCGGC-----	
gp160 del V1-2	(521)	-----	
gp 160 del 128-194	(521)	-----	
gp140TM	(521)	GCAGCTTCAACATCACCACCAGCGTGCGCGACAAGGTGCA	
gp140	(521)	GCAGCTTCAACATCACCACCAGCGTGCGCGACAAGGTGCA	
gp140mut	(521)	GCAGCTTCAACATCACCACCAGCGTGCGCGACAAGGTGCA	
gp120	(521)	GCAGCTTCAACATCACCACCAGCGTGCGCGACAAGGTGCA	
Consensus	(521)	GCAGCTTCAACATCACCACCAGCGTGCGCGACAAGGTGCA	

FIG. 66B-3

SUBSTITUTE SHEET (RULE 26)

100 / 131

		561	600
gp160	(561)	GAAGGAGTACAGCCTGTTCTACAAGCTGGACGTGGTGCCC	
gp160 del V1	(465)	GAAGGAGTACAGCCTGTTCTACAAGCTGGACGTGGTGCCC	
gp160 del V2	(544)	-----	
gp160 del V1-2	(364)	-----	
gp 160 del 128-194	(385)	-----	
gp140TM	(561)	GAAGGAGTACAGCCTGTTCTACAAGCTGGACGTGGTGCCC	
gp140	(561)	GAAGGAGTACAGCCTGTTCTACAAGCTGGACGTGGTGCCC	
gp140mut	(561)	GAAGGAGTACAGCCTGTTCTACAAGCTGGACGTGGTGCCC	
gp120	(561)	GAAGGAGTACAGCCTGTTCTACAAGCTGGACGTGGTGCCC	
Consensus	(561)	GAAGGAGTACAGCCTGTTCTACAAGCTGGACGTGGTGCCC	640
		601	
gp160	(601)	ATCGACAACGACAACGCCAGCTACCGCCTGATCAACTGCA	
gp160 del V1	(505)	ATCGACAACGACAACGCCAGCTACCGCCTGATCAACTGCA	
gp160 del V2	(544)	-----CGCCTGATCAACTGCA	
gp160 del V1-2	(364)	-----	
gp 160 del 128-194	(385)	-----AACTGCG	
gp140TM	(601)	ATCGACAACGACAACGCCAGCTACCGCCTGATCAACTGCA	
gp140	(601)	ATCGACAACGACAACGCCAGCTACCGCCTGATCAACTGCA	
gp140mut	(601)	ATCGACAACGACAACGCCAGCTACCGCCTGATCAACTGCA	
gp120	(601)	ATCGACAACGACAACGCCAGCTACCGCCTGATCAACTGCA	
Consensus	(601)	ATCGACAACGACAACGCCAGCTACCGCCTGATCAACTGCA	680
		641	
gp160	(641)	ACACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTT	
gp160 del V1	(545)	ACACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTT	
gp160 del V2	(560)	ACACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTT	
gp160 del V1-2	(364)	-----CAGGCCTGCCCCAAGGTGAGCTT	
gp 160 del 128-194	(392)	AGACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTT	
gp140TM	(641)	ACACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTT	
gp140	(641)	ACACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTT	
gp140mut	(641)	ACACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTT	
gp120	(641)	ACACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTT	
Consensus	(641)	ACACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTT	720
		681	
gp160	(681)	CGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTTC	
gp160 del V1	(585)	CGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTTC	
gp160 del V2	(600)	CGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTTC	
gp160 del V1-2	(387)	CGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTTC	
gp 160 del 128-194	(432)	CGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTTC	
gp140TM	(681)	CGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTTC	
gp140	(681)	CGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTTC	
gp140mut	(681)	CGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTTC	
gp120	(681)	CGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTTC	
Consensus	(681)	CGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTTC	760
		721	
gp160	(721)	GCCATCCTGAAGTGCAAGGACAAGAAGTTCAACGGCACCG	
gp160 del V1	(625)	GCCATCCTGAAGTGCAAGGACAAGAAGTTCAACGGCACCG	
gp160 del V2	(640)	GCCATCCTGAAGTGCAAGGACAAGAAGTTCAACGGCACCG	
gp160 del V1-2	(427)	GCCATCCTGAAGTGCAAGGACAAGAAGTTCAACGGCACCG	
gp 160 del 128-194	(472)	GCCATCCTGAAGTGCAAGGACAAGAAGTTCAACGGCACCG	
gp140TM	(721)	GCCATCCTGAAGTGCAAGGACAAGAAGTTCAACGGCACCG	
gp140	(721)	GCCATCCTGAAGTGCAAGGACAAGAAGTTCAACGGCACCG	
gp140mut	(721)	GCCATCCTGAAGTGCAAGGACAAGAAGTTCAACGGCACCG	
gp120	(721)	GCCATCCTGAAGTGCAAGGACAAGAAGTTCAACGGCACCG	
Consensus	(721)	GCCATCCTGAAGTGCAAGGACAAGAAGTTCAACGGCACCG	

FIG. 66B-4

SUBSTITUTE SHEET (RULE 26)

101 / 131

	761	800
gp160	(761) GCCCCTGCAAGAACGTGAGCACCGTGCAAGTGCACCCACGG	
gp160 del V1	(665) GCCCCTGCAAGAACGTGAGCACCGTGCAAGTGCACCCACGG	
gp160 del V2	(680) GCCCCTGCAAGAACGTGAGCACCGTGCAAGTGCACCCACGG	
gp160 del V1-2	(467) GCCCCTGCAAGAACGTGAGCACCGTGCAAGTGCACCCACGG	
gp 160 del 128-194	(512) GCCCCTGCAAGAACGTGAGCACCGTGCAAGTGCACCCACGG	
gp140TM	(761) GCCCCTGCAAGAACGTGAGCACCGTGCAAGTGCACCCACGG	
gp140	(761) GCCCCTGCAAGAACGTGAGCACCGTGCAAGTGCACCCACGG	
gp140mut	(761) GCCCCTGCAAGAACGTGAGCACCGTGCAAGTGCACCCACGG	
gp120	(761) GCCCCTGCAAGAACGTGAGCACCGTGCAAGTGCACCCACGG	
Consensus	(761) GCCCCTGCAAGAACGTGAGCACCGTGCAAGTGCACCCACGG	
	801	840
gp160	(801) CATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGC	
gp160 del V1	(705) CATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGC	
gp160 del V2	(720) CATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGC	
gp160 del V1-2	(507) CATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGC	
gp 160 del 128-194	(552) CATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGC	
gp140TM	(801) CATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGC	
gp140	(801) CATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGC	
gp140mut	(801) CATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGC	
gp120	(801) CATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGC	
Consensus	(801) CATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGC	
	841	880
gp160	(841) AGCCTGGCCGAGGAGGAGATCGTGCTGCGCTCCGAGAACT	
gp160 del V1	(745) AGCCTGGCCGAGGAGGAGATCGTGCTGCGCTCCGAGAACT	
gp160 del V2	(760) AGCCTGGCCGAGGAGGAGATCGTGCTGCGCTCCGAGAACT	
gp160 del V1-2	(547) AGCCTGGCCGAGGAGGAGATCGTGCTGCGCTCCGAGAACT	
gp 160 del 128-194	(592) AGCCTGGCCGAGGAGGAGATCGTGCTGCGCTCCGAGAACT	
gp140TM	(841) AGCCTGGCCGAGGAGGAGATCGTGCTGCGCTCCGAGAACT	
gp140	(841) AGCCTGGCCGAGGAGGAGATCGTGCTGCGCTCCGAGAACT	
gp140mut	(841) AGCCTGGCCGAGGAGGAGATCGTGCTGCGCTCCGAGAACT	
gp120	(841) AGCCTGGCCGAGGAGGAGATCGTGCTGCGCTCCGAGAACT	
Consensus	(841) AGCCTGGCCGAGGAGGAGATCGTGCTGCGCTCCGAGAACT	
	881	920
gp160	(881) TCACCGACAACGCCAAGACCATCATCGTGCAAGTGCACCTGAACGA	
gp160 del V1	(785) TCACCGACAACGCCAAGACCATCATCGTGCAAGTGCACCTGAACGA	
gp160 del V2	(800) TCACCGACAACGCCAAGACCATCATCGTGCAAGTGCACCTGAACGA	
gp160 del V1-2	(587) TCACCGACAACGCCAAGACCATCATCGTGCAAGTGCACCTGAACGA	
gp 160 del 128-194	(632) TCACCGACAACGCCAAGACCATCATCGTGCAAGTGCACCTGAACGA	
gp140TM	(881) TCACCGACAACGCCAAGACCATCATCGTGCAAGTGCACCTGAACGA	
gp140	(881) TCACCGACAACGCCAAGACCATCATCGTGCAAGTGCACCTGAACGA	
gp140mut	(881) TCACCGACAACGCCAAGACCATCATCGTGCAAGTGCACCTGAACGA	
gp120	(881) TCACCGACAACGCCAAGACCATCATCGTGCAAGTGCACCTGAACGA	
Consensus	(881) TCACCGACAACGCCAAGACCATCATCGTGCAAGTGCACCTGAACGA	
	921	960
gp160	(921) GTCCGTGGAGATCAACTGCATCCGCCCCCAACAACAACACG	
gp160 del V1	(825) GTCCGTGGAGATCAACTGCATCCGCCCCCAACAACAACACG	
gp160 del V2	(840) GTCCGTGGAGATCAACTGCATCCGCCCCCAACAACAACACG	
gp160 del V1-2	(627) GTCCGTGGAGATCAACTGCATCCGCCCCCAACAACAACACG	
gp 160 del 128-194	(672) GTCCGTGGAGATCAACTGCATCCGCCCCCAACAACAACACG	
gp140TM	(921) GTCCGTGGAGATCAACTGCATCCGCCCCCAACAACAACACG	
gp140	(921) GTCCGTGGAGATCAACTGCATCCGCCCCCAACAACAACACG	
gp140mut	(921) GTCCGTGGAGATCAACTGCATCCGCCCCCAACAACAACACG	
gp120	(921) GTCCGTGGAGATCAACTGCATCCGCCCCCAACAACAACACG	
Consensus	(921) GTCCGTGGAGATCAACTGCATCCGCCCCCAACAACAACACG	

FIG. 66B-5

SUBSTITUTE SHEET (RULE 26)

102 / 131

		961	1000
gp160	(961)	CGTAAGAGCATCCACATCGGCCCCGGCCGCGCCTTCTACG	
gp160 del V1	(865)	CGTAAGAGCATCCACATCGGCCCCGGCCGCGCCTTCTACG	
gp160 del V2	(880)	CGTAAGAGCATCCACATCGGCCCCGGCCGCGCCTTCTACG	
gp160 del V1-2	(667)	CGTAAGAGCATCCACATCGGCCCCGGCCGCGCCTTCTACG	
gp 160 del 128-194	(712)	CGTAAGAGCATCCACATCGGCCCCGGCCGCGCCTTCTACG	
gp140TM	(961)	CGTAAGAGCATCCACATCGGCCCCGGCCGCGCCTTCTACG	
gp140	(961)	CGTAAGAGCATCCACATCGGCCCCGGCCGCGCCTTCTACG	
gp140mut	(961)	CGTAAGAGCATCCACATCGGCCCCGGCCGCGCCTTCTACG	
gp120	(961)	CGTAAGAGCATCCACATCGGCCCCGGCCGCGCCTTCTACG	
Consensus	(961)	CGTAAGAGCATCCACATCGGCCCCGGCCGCGCCTTCTACG	
		1001	1040
gp160	(1001)	CCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTG	
gp160 del V1	(905)	CCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTG	
gp160 del V2	(920)	CCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTG	
gp160 del V1-2	(707)	CCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTG	
gp 160 del 128-194	(752)	CCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTG	
gp140TM	(1001)	CCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTG	
gp140	(1001)	CCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTG	
gp140mut	(1001)	CCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTG	
gp120	(1001)	CCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTG	
Consensus	(1001)	CCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTG	
		1041	1080
gp160	(1041)	CAACATCAGCAAGGCCAACTGGACCAACACCCTCGAGCAG	
gp160 del V1	(945)	CAACATCAGCAAGGCCAACTGGACCAACACCCTCGAGCAG	
gp160 del V2	(960)	CAACATCAGCAAGGCCAACTGGACCAACACCCTCGAGCAG	
gp160 del V1-2	(747)	CAACATCAGCAAGGCCAACTGGACCAACACCCTCGAGCAG	
gp 160 del 128-194	(792)	CAACATCAGCAAGGCCAACTGGACCAACACCCTCGAGCAG	
gp140TM	(1041)	CAACATCAGCAAGGCCAACTGGACCAACACCCTCGAGCAG	
gp140	(1041)	CAACATCAGCAAGGCCAACTGGACCAACACCCTCGAGCAG	
gp140mut	(1041)	CAACATCAGCAAGGCCAACTGGACCAACACCCTCGAGCAG	
gp120	(1041)	CAACATCAGCAAGGCCAACTGGACCAACACCCTCGAGCAG	
Consensus	(1041)	CAACATCAGCAAGGCCAACTGGACCAACACCCTCGAGCAG	
		1081	1120
gp160	(1081)	ATCGTGGAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGA	
gp160 del V1	(985)	ATCGTGGAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGA	
gp160 del V2	(1000)	ATCGTGGAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGA	
gp160 del V1-2	(787)	ATCGTGGAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGA	
gp 160 del 128-194	(832)	ATCGTGGAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGA	
gp140TM	(1081)	ATCGTGGAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGA	
gp140	(1081)	ATCGTGGAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGA	
gp140mut	(1081)	ATCGTGGAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGA	
gp120	(1081)	ATCGTGGAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGA	
Consensus	(1081)	ATCGTGGAGAAGCTGCGCGAGCAGTTCGGCAACAACAAGA	
		1121	1160
gp160	(1121)	CCATCATCTTCAACAGCAGCAGCGGCGGCGACCCCGAGAT	
gp160 del V1	(1025)	CCATCATCTTCAACAGCAGCAGCGGCGGCGACCCCGAGAT	
gp160 del V2	(1040)	CCATCATCTTCAACAGCAGCAGCGGCGGCGACCCCGAGAT	
gp160 del V1-2	(827)	CCATCATCTTCAACAGCAGCAGCGGCGGCGACCCCGAGAT	
gp 160 del 128-194	(872)	CCATCATCTTCAACAGCAGCAGCGGCGGCGACCCCGAGAT	
gp140TM	(1121)	CCATCATCTTCAACAGCAGCAGCGGCGGCGACCCCGAGAT	
gp140	(1121)	CCATCATCTTCAACAGCAGCAGCGGCGGCGACCCCGAGAT	
gp140mut	(1121)	CCATCATCTTCAACAGCAGCAGCGGCGGCGACCCCGAGAT	
gp120	(1121)	CCATCATCTTCAACAGCAGCAGCGGCGGCGACCCCGAGAT	
Consensus	(1121)	CCATCATCTTCAACAGCAGCAGCGGCGGCGACCCCGAGAT	

FIG. 66B-6

SUBSTITUTE SHEET (RULE 26)

103 / 131

		1161	1200
gp160	(1161)	CGTGTTCCACAGCTTCAACTGCGGCGGCGAGTTCTTCTAC	
gp160 del V1	(1065)	CGTGTTCCACAGCTTCAACTGCGGCGGCGAGTTCTTCTAC	
gp160 del V2	(1080)	CGTGTTCCACAGCTTCAACTGCGGCGGCGAGTTCTTCTAC	
gp160 del V1-2	(867)	CGTGTTCCACAGCTTCAACTGCGGCGGCGAGTTCTTCTAC	
gp 160 del 128-194	(912)	CGTGTTCCACAGCTTCAACTGCGGCGGCGAGTTCTTCTAC	
gp140TM	(1161)	CGTGTTCCACAGCTTCAACTGCGGCGGCGAGTTCTTCTAC	
gp140	(1161)	CGTGTTCCACAGCTTCAACTGCGGCGGCGAGTTCTTCTAC	
gp140mut	(1161)	CGTGTTCCACAGCTTCAACTGCGGCGGCGAGTTCTTCTAC	
gp120	(1161)	CGTGTTCCACAGCTTCAACTGCGGCGGCGAGTTCTTCTAC	
Consensus	(1161)	CGTGTTCCACAGCTTCAACTGCGGCGGCGAGTTCTTCTAC	
		1240	
gp160	(1201)	TGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCA	
gp160 del V1	(1105)	TGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCA	
gp160 del V2	(1120)	TGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCA	
gp160 del V1-2	(907)	TGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCA	
gp 160 del 128-194	(952)	TGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCA	
gp140TM	(1201)	TGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCA	
gp140	(1201)	TGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCA	
gp140mut	(1201)	TGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCA	
gp120	(1201)	TGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCA	
Consensus	(1201)	TGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCA	
		1241	1280
gp160	(1241)	CCGAGGAGGTGAACAAGACCAAGGAGAACGACACCATCAT	
gp160 del V1	(1145)	CCGAGGAGGTGAACAAGACCAAGGAGAACGACACCATCAT	
gp160 del V2	(1160)	CCGAGGAGGTGAACAAGACCAAGGAGAACGACACCATCAT	
gp160 del V1-2	(947)	CCGAGGAGGTGAACAAGACCAAGGAGAACGACACCATCAT	
gp 160 del 128-194	(992)	CCGAGGAGGTGAACAAGACCAAGGAGAACGACACCATCAT	
gp140TM	(1241)	CCGAGGAGGTGAACAAGACCAAGGAGAACGACACCATCAT	
gp140	(1241)	CCGAGGAGGTGAACAAGACCAAGGAGAACGACACCATCAT	
gp140mut	(1241)	CCGAGGAGGTGAACAAGACCAAGGAGAACGACACCATCAT	
gp120	(1241)	CCGAGGAGGTGAACAAGACCAAGGAGAACGACACCATCAT	
Consensus	(1241)	CCGAGGAGGTGAACAAGACCAAGGAGAACGACACCATCAT	
		1320	
gp160	(1281)	CCTGCCCTGCCGCATCCGCCAGATCATCAACATGTGGCAG	
gp160 del V1	(1185)	CCTGCCCTGCCGCATCCGCCAGATCATCAACATGTGGCAG	
gp160 del V2	(1200)	CCTGCCCTGCCGCATCCGCCAGATCATCAACATGTGGCAG	
gp160 del V1-2	(987)	CCTGCCCTGCCGCATCCGCCAGATCATCAACATGTGGCAG	
gp 160 del 128-194	(1032)	CCTGCCCTGCCGCATCCGCCAGATCATCAACATGTGGCAG	
gp140TM	(1281)	CCTGCCCTGCCGCATCCGCCAGATCATCAACATGTGGCAG	
gp140	(1281)	CCTGCCCTGCCGCATCCGCCAGATCATCAACATGTGGCAG	
gp140mut	(1281)	CCTGCCCTGCCGCATCCGCCAGATCATCAACATGTGGCAG	
gp120	(1281)	CCTGCCCTGCCGCATCCGCCAGATCATCAACATGTGGCAG	
Consensus	(1281)	CCTGCCCTGCCGCATCCGCCAGATCATCAACATGTGGCAG	
		1321	1360
gp160	(1321)	GAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCC	
gp160 del V1	(1225)	GAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCC	
gp160 del V2	(1240)	GAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCC	
gp160 del V1-2	(1027)	GAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCC	
gp 160 del 128-194	(1072)	GAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCC	
gp140TM	(1321)	GAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCC	
gp140	(1321)	GAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCC	
gp140mut	(1321)	GAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCC	
gp120	(1321)	GAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCC	
Consensus	(1321)	GAGGTGGGCAAGGCCATGTACGCCCCCCCCATCCGCGGCC	

FIG. 66B-7

104 / 131

		1361	1400
gp160	(1361)	AGATCAAGTGCAGCAGCAATATTACCGGCCTGCTGCTGAC	
gp160 del V1	(1265)	AGATCAAGTGCAGCAGCAATATTACCGGCCTGCTGCTGAC	
gp160 del V2	(1280)	AGATCAAGTGCAGCAGCAATATTACCGGCCTGCTGCTGAC	
gp160 del V1-2	(1067)	AGATCAAGTGCAGCAGCAATATTACCGGCCTGCTGCTGAC	
gp 160 del 128-194	(1112)	AGATCAAGTGCAGCAGCAATATTACCGGCCTGCTGCTGAC	
gp140TM	(1361)	AGATCAAGTGCAGCAGCAATATTACCGGCCTGCTGCTGAC	
gp140	(1361)	AGATCAAGTGCAGCAGCAATATTACCGGCCTGCTGCTGAC	
gp140mut	(1361)	AGATCAAGTGCAGCAGCAATATTACCGGCCTGCTGCTGAC	
gp120	(1361)	AGATCAAGTGCAGCAGCAATATTACCGGCCTGCTGCTGAC	
Consensus	(1361)	AGATCAAGTGCAGCAGCAATATTACCGGCCTGCTGCTGAC	
		1401	1440
gp160	(1401)	CCGCGACGGCGGCACCAACAACAACCGCACCAACGACACC	
gp160 del V1	(1305)	CCGCGACGGCGGCACCAACAACAACCGCACCAACGACACC	
gp160 del V2	(1320)	CCGCGACGGCGGCACCAACAACAACCGCACCAACGACACC	
gp160 del V1-2	(1107)	CCGCGACGGCGGCACCAACAACAACCGCACCAACGACACC	
gp 160 del 128-194	(1152)	CCGCGACGGCGGCACCAACAACAACCGCACCAACGACACC	
gp140TM	(1401)	CCGCGACGGCGGCACCAACAACAACCGCACCAACGACACC	
gp140	(1401)	CCGCGACGGCGGCACCAACAACAACCGCACCAACGACACC	
gp140mut	(1401)	CCGCGACGGCGGCACCAACAACAACCGCACCAACGACACC	
gp120	(1401)	CCGCGACGGCGGCACCAACAACAACCGCACCAACGACACC	
Consensus	(1401)	CCGCGACGGCGGCACCAACAACAACCGCACCAACGACACC	
		1441	1480
gp160	(1441)	GAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAAC	
gp160 del V1	(1345)	GAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAAC	
gp160 del V2	(1360)	GAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAAC	
gp160 del V1-2	(1147)	GAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAAC	
gp 160 del 128-194	(1192)	GAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAAC	
gp140TM	(1441)	GAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAAC	
gp140	(1441)	GAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAAC	
gp140mut	(1441)	GAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAAC	
gp120	(1441)	GAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAAC	
Consensus	(1441)	GAGACCTTCCGCCCCGGCGGCGGCAACATGAAGGACAAC	
		1481	1520
gp160	(1481)	GGCGCAGCGAGCTGTACAAGTACAAGGTGGTGCGCATCGA	
gp160 del V1	(1385)	GGCGCAGCGAGCTGTACAAGTACAAGGTGGTGCGCATCGA	
gp160 del V2	(1400)	GGCGCAGCGAGCTGTACAAGTACAAGGTGGTGCGCATCGA	
gp160 del V1-2	(1187)	GGCGCAGCGAGCTGTACAAGTACAAGGTGGTGCGCATCGA	
gp 160 del 128-194	(1232)	GGCGCAGCGAGCTGTACAAGTACAAGGTGGTGCGCATCGA	
gp140TM	(1481)	GGCGCAGCGAGCTGTACAAGTACAAGGTGGTGCGCATCGA	
gp140	(1481)	GGCGCAGCGAGCTGTACAAGTACAAGGTGGTGCGCATCGA	
gp140mut	(1481)	GGCGCAGCGAGCTGTACAAGTACAAGGTGGTGCGCATCGA	
gp120	(1481)	GGCGCAGCGAGCTGTACAAGTACAAGGTGGTGCGCATCGA	
Consensus	(1481)	GGCGCAGCGAGCTGTACAAGTACAAGGTGGTGCGCATCGA	
		1521	1560
gp160	(1521)	GCCCCCTGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTG	
gp160 del V1	(1425)	GCCCCCTGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTG	
gp160 del V2	(1440)	GCCCCCTGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTG	
gp160 del V1-2	(1227)	GCCCCCTGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTG	
gp 160 del 128-194	(1272)	GCCCCCTGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTG	
gp140TM	(1521)	GCCCCCTGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTG	
gp140	(1521)	GCCCCCTGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTG	
gp140mut	(1521)	GCCCCCTGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTG	
gp120	(1521)	GCCCCCTGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTG	
Consensus	(1521)	GCCCCCTGGGCGTGGCCCCCACCAGGCCAAGCGCCGCGTG	

FIG. 66B-8

SUBSTITUTE SHEET (RULE 26)

105 / 131

		1561	1600
gp160	(1561)	GTGCAGCGCGAGAAGCGCGCCGTGGGCCTGGGCGCCCTGT	
gp160 del V1	(1465)	GTGCAGCGCGAGAAGCGCGCCGTGGGCCTGGGCGCCCTGT	
gp160 del V2	(1480)	GTGCAGCGCGAGAAGCGCGCCGTGGGCCTGGGCGCCCTGT	
gp160 del V1-2	(1267)	GTGCAGCGCGAGAAGCGCGCCGTGGGCCTGGGCGCCCTGT	
gp 160 del 128-194	(1312)	GTGCAGCGCGAGAAGCGCGCCGTGGGCCTGGGCGCCCTGT	
gp140TM	(1561)	GTGCAGCGCGAGAAGCGCGCCGTGGGCCTGGGCGCCCTGT	
gp140	(1561)	GTGCAGCGCGAGAAGCGCGCCGTGGGCCTGGGCGCCCTGT	
gp140mut	(1561)	GTGCAGCGCGAGAAGAGCGCCGTGGGCCTGGGCGCCCTGT	
gp120	(1561)	GTGCAGCGCGAGAAGCGCTAAG-----	
Consensus	(1561)	GTGCAGCGCGAGAAGCGCGCCGTGGGCCTGGGCGCCCTGT	
		1601	1640
gp160	(1601)	TCATCGGCTTC-CTGGGCGCCGCCGGGAGCACCATGGGCG	
gp160 del V1	(1505)	TCATCGGCTTC-CTGGGCGCCGCCGGGAGCACCATGGGCG	
gp160 del V2	(1520)	TCATCGGCTTC-CTGGGCGCCGCCGGGAGCACCATGGGCG	
gp160 del V1-2	(1307)	TCATCGGCTTC-CTGGGCGCCGCCGGGAGCACCATGGGCG	
gp 160 del 128-194	(1352)	TCATCGGCTTC-CTGGGCGCCGCCGGGAGCACCATGGGCG	
gp140TM	(1601)	TCATCGGCTTC-CTGGGCGCCGCCGGGAGCACCATGGGCG	
gp140	(1601)	TCATCGGCTTC-CTGGGCGCCGCCGGGAGCACCATGGGCG	
gp140mut	(1601)	TCATCGGCTTC-CTGGGCGCCGCCGGGAGCACCATGGGCG	
gp120	(1583)	ATATCGGATCCTCTAGA-----	
Consensus	(1601)	TCATCGGCTTCNCTGGGCGCCGCCGGGAGCACCATGGGCG	
		1641	1680
gp160	(1640)	CCGCCTCCGTGACCCTGACCGTGCAGGCCCGCCAGCTGCT	
gp160 del V1	(1544)	CCGCCTCCGTGACCCTGACCGTGCAGGCCCGCCAGCTGCT	
gp160 del V2	(1559)	CCGCCTCCGTGACCCTGACCGTGCAGGCCCGCCAGCTGCT	
gp160 del V1-2	(1346)	CCGCCTCCGTGACCCTGACCGTGCAGGCCCGCCAGCTGCT	
gp 160 del 128-194	(1391)	CCGCCTCCGTGACCCTGACCGTGCAGGCCCGCCAGCTGCT	
gp140TM	(1640)	CCGCCTCCGTGACCCTGACCGTGCAGGCCCGCCAGCTGCT	
gp140	(1640)	CCGCCTCCGTGACCCTGACCGTGCAGGCCCGCCAGCTGCT	
gp140mut	(1640)	CCGCCTCCGTGACCCTGACCGTGCAGGCCCGCCAGCTGCT	
gp120	(1600)	-----	
Consensus	(1641)	CCGCCTCCGTGACCCTGACCGTGCAGGCCCGCCAGCTGCT	
		1681	1720
gp160	(1680)	GAGCGGCATCGTGCAGCAGCAGAACAACCTGCTGCGCGCC	
gp160 del V1	(1584)	GAGCGGCATCGTGCAGCAGCAGAACAACCTGCTGCGCGCC	
gp160 del V2	(1599)	GAGCGGCATCGTGCAGCAGCAGAACAACCTGCTGCGCGCC	
gp160 del V1-2	(1386)	GAGCGGCATCGTGCAGCAGCAGAACAACCTGCTGCGCGCC	
gp 160 del 128-194	(1431)	GAGCGGCATCGTGCAGCAGCAGAACAACCTGCTGCGCGCC	
gp140TM	(1680)	GAGCGGCATCGTGCAGCAGCAGAACAACCTGCTGCGCGCC	
gp140	(1680)	GAGCGGCATCGTGCAGCAGCAGAACAACCTGCTGCGCGCC	
gp140mut	(1680)	GAGCGGCATCGTGCAGCAGCAGAACAACCTGCTGCGCGCC	
gp120	(1600)	-----	
Consensus	(1681)	GAGCGGCATCGTGCAGCAGCAGAACAACCTGCTGCGCGCC	
		1721	1760
gp160	(1720)	ATCGAGGCCAGCAGCACCTGCTGCAGCTGACCGTGTGGG	
gp160 del V1	(1624)	ATCGAGGCCAGCAGCACCTGCTGCAGCTGACCGTGTGGG	
gp160 del V2	(1639)	ATCGAGGCCAGCAGCACCTGCTGCAGCTGACCGTGTGGG	
gp160 del V1-2	(1426)	ATCGAGGCCAGCAGCACCTGCTGCAGCTGACCGTGTGGG	
gp 160 del 128-194	(1471)	ATCGAGGCCAGCAGCACCTGCTGCAGCTGACCGTGTGGG	
gp140TM	(1720)	ATCGAGGCCAGCAGCACCTGCTGCAGCTGACCGTGTGGG	
gp140	(1720)	ATCGAGGCCAGCAGCACCTGCTGCAGCTGACCGTGTGGG	
gp140mut	(1720)	ATCGAGGCCAGCAGCACCTGCTGCAGCTGACCGTGTGGG	
gp120	(1600)	-----	
Consensus	(1721)	ATCGAGGCCAGCAGCACCTGCTGCAGCTGACCGTGTGGG	

FIG. 66B-9

SUBSTITUTE SHEET (RULE 26)

106/131

		1761	1800
gp160	(1760)	GCATCAAGCAGCTGCAGGCCCCGCATCCTGGCCGTGGAGCG	
gp160 del V1	(1664)	GCATCAAGCAGCTGCAGGCCCCGCATCCTGGCCGTGGAGCG	
gp160 del V2	(1679)	GCATCAAGCAGCTGCAGGCCCCGCATCCTGGCCGTGGAGCG	
gp160 del V1-2	(1466)	GCATCAAGCAGCTGCAGGCCCCGCATCCTGGCCGTGGAGCG	
gp 160 del 128-194	(1511)	GCATCAAGCAGCTGCAGGCCCCGCATCCTGGCCGTGGAGCG	
gp140TM	(1760)	GCATCAAGCAGCTGCAGGCCCCGCATCCTGGCCGTGGAGCG	
gp140	(1760)	GCATCAAGCAGCTGCAGGCCCCGCATCCTGGCCGTGGAGCG	
gp140mut	(1760)	GCATCAAGCAGCTGCAGGCCCCGCATCCTGGCCGTGGAGCG	
gp120	(1600)	-----	
Consensus	(1761)	GCATCAAGCAGCTGCAGGCCCCGCATCCTGGCCGTGGAGCG	
		1801	1840
gp160	(1800)	CTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGC	
gp160 del V1	(1704)	CTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGC	
gp160 del V2	(1719)	CTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGC	
gp160 del V1-2	(1506)	CTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGC	
gp 160 del 128-194	(1551)	CTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGC	
gp140TM	(1800)	CTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGC	
gp140	(1800)	CTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGC	
gp140mut	(1800)	CTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGC	
gp120	(1600)	-----	
Consensus	(1801)	CTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGC	
		1841	1880
gp160	(1840)	AGCGGCAAGCTGATCTGCACCACCACCGTGCCCTGGAACA	
gp160 del V1	(1744)	AGCGGCAAGCTGATCTGCACCACCACCGTGCCCTGGAACA	
gp160 del V2	(1759)	AGCGGCAAGCTGATCTGCACCACCACCGTGCCCTGGAACA	
gp160 del V1-2	(1546)	AGCGGCAAGCTGATCTGCACCACCACCGTGCCCTGGAACA	
gp 160 del 128-194	(1591)	AGCGGCAAGCTGATCTGCACCACCACCGTGCCCTGGAACA	
gp140TM	(1840)	AGCGGCAAGCTGATCTGCACCACCACCGTGCCCTGGAACA	
gp140	(1840)	AGCGGCAAGCTGATCTGCACCACCACCGTGCCCTGGAACA	
gp140mut	(1840)	AGCGGCAAGCTGATCTGCACCACCACCGTGCCCTGGAACA	
gp120	(1600)	-----	
Consensus	(1841)	AGCGGCAAGCTGATCTGCACCACCACCGTGCCCTGGAACA	
		1881	1920
gp160	(1880)	GCAGCTGGAGCAACAAGAGCCTGACCGAGATCTGGGACAA	
gp160 del V1	(1784)	GCAGCTGGAGCAACAAGAGCCTGACCGAGATCTGGGACAA	
gp160 del V2	(1799)	GCAGCTGGAGCAACAAGAGCCTGACCGAGATCTGGGACAA	
gp160 del V1-2	(1586)	GCAGCTGGAGCAACAAGAGCCTGACCGAGATCTGGGACAA	
gp 160 del 128-194	(1631)	GCAGCTGGAGCAACAAGAGCCTGACCGAGATCTGGGACAA	
gp140TM	(1880)	GCAGCTGGAGCAACAAGAGCCTGACCGAGATCTGGGACAA	
gp140	(1880)	GCAGCTGGAGCAACAAGAGCCTGACCGAGATCTGGGACAA	
gp140mut	(1880)	GCAGCTGGAGCAACAAGAGCCTGACCGAGATCTGGGACAA	
gp120	(1600)	-----	
Consensus	(1881)	GCAGCTGGAGCAACAAGAGCCTGACCGAGATCTGGGACAA	
		1921	1960
gp160	(1920)	CATGACCTGGATGGAGTGGGAGCGCGAGATCGGCAACTAC	
gp160 del V1	(1824)	CATGACCTGGATGGAGTGGGAGCGCGAGATCGGCAACTAC	
gp160 del V2	(1839)	CATGACCTGGATGGAGTGGGAGCGCGAGATCGGCAACTAC	
gp160 del V1-2	(1626)	CATGACCTGGATGGAGTGGGAGCGCGAGATCGGCAACTAC	
gp 160 del 128-194	(1671)	CATGACCTGGATGGAGTGGGAGCGCGAGATCGGCAACTAC	
gp140TM	(1920)	CATGACCTGGATGGAGTGGGAGCGCGAGATCGGCAACTAC	
gp140	(1920)	CATGACCTGGATGGAGTGGGAGCGCGAGATCGGCAACTAC	
gp140mut	(1920)	CATGACCTGGATGGAGTGGGAGCGCGAGATCGGCAACTAC	
gp120	(1600)	-----	
Consensus	(1921)	CATGACCTGGATGGAGTGGGAGCGCGAGATCGGCAACTAC	

FIG. 66B-10

SUBSTITUTE SHEET (RULE 26)

107 / 131

		1961	2000
gp160	(1960)	ACCGGCCTGATCTACAACCTGATCGAGATCGCCCAGAACC	
gp160 del V1	(1864)	ACCGGCCTGATCTACAACCTGATCGAGATCGCCCAGAACC	
gp160 del V2	(1879)	ACCGGCCTGATCTACAACCTGATCGAGATCGCCCAGAACC	
gp160 del V1-2	(1666)	ACCGGCCTGATCTACAACCTGATCGAGATCGCCCAGAACC	
gp 160 del 128-194	(1711)	ACCGGCCTGATCTACAACCTGATCGAGATCGCCCAGAACC	
gp140TM	(1960)	ACCGGCCTGATCTACAACCTGATCGAGATCGCCCAGAACC	
gp140	(1960)	ACCGGCCTGATCTACAACCTGATCGAGATCGCCCAGAACC	
gp140mut	(1960)	ACCGGCCTGATCTACAACCTGATCGAGATCGCCCAGAACC	
gp120	(1600)	-----	
Consensus	(1961)	ACCGGCCTGATCTACAACCTGATCGAGATCGCCCAGAACC	
		2001	2040
gp160	(2000)	AGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAA	
gp160 del V1	(1904)	AGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAA	
gp160 del V2	(1919)	AGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAA	
gp160 del V1-2	(1706)	AGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAA	
gp 160 del 128-194	(1751)	AGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAA	
gp140TM	(2000)	AGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAA	
gp140	(2000)	AGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAA	
gp140mut	(2000)	AGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAA	
gp120	(1600)	-----	
Consensus	(2001)	AGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAA	
		2041	2080
gp160	(2040)	GTGGGCCAGCCTGTGGAACCTGGTTCGACATCACCAACTGG	
gp160 del V1	(1944)	GTGGGCCAGCCTGTGGAACCTGGTTCGACATCACCAACTGG	
gp160 del V2	(1959)	GTGGGCCAGCCTGTGGAACCTGGTTCGACATCACCAACTGG	
gp160 del V1-2	(1746)	GTGGGCCAGCCTGTGGAACCTGGTTCGACATCACCAACTGG	
gp 160 del 128-194	(1791)	GTGGGCCAGCCTGTGGAACCTGGTTCGACATCACCAACTGG	
gp140TM	(2040)	GTGGGCCAGCCTGTGGAACCTGGTTCGACATCACCAACTGG	
gp140	(2040)	GTGGGCCAGCCTGTGGAACCTGGTTCGACATCACCAACTGG	
gp140mut	(2040)	GTGGGCCAGCCTGTGGAACCTGGTTCGACATCACCAACTGG	
gp120	(1600)	-----	
Consensus	(2041)	GTGGGCCAGCCTGTGGAACCTGGTTCGACATCACCAACTGG	
		2081	2120
gp160	(2080)	CTGTGGTACATCCGCATCTTCATCATGATCGTGGGCGGCC	
gp160 del V1	(1984)	CTGTGGTACATCCGCATCTTCATCATGATCGTGGGCGGCC	
gp160 del V2	(1999)	CTGTGGTACATCCGCATCTTCATCATGATCGTGGGCGGCC	
gp160 del V1-2	(1786)	CTGTGGTACATCCGCATCTTCATCATGATCGTGGGCGGCC	
gp 160 del 128-194	(1831)	CTGTGGTACATCCGCATCTTCATCATGATCGTGGGCGGCC	
gp140TM	(2080)	CTGTGGTACATCCGCATCTTCATCATGATCGTGGGCGGCC	
gp140	(2080)	CTGTGGTACATC-----	
gp140mut	(2080)	CTGTGGTACATC-----	
gp120	(1600)	-----	
Consensus	(2081)	CTGTGGTACATCCGCATCTTCATCATGATCGTGGGCGGCC	
		2121	2160
gp160	(2120)	TGATCGGCCTGCGCATCGTGTTCCGCGTGCTGAGCA----	
gp160 del V1	(2024)	TGATCGGCCTGCGCATCGTGTTCCGCGTGCTGAGCA----	
gp160 del V2	(2039)	TGATCGGCCTGCGCATCGTGTTCCGCGTGCTGAGCA----	
gp160 del V1-2	(1826)	TGATCGGCCTGCGCATCGTGTTCCGCGTGCTGAGCA----	
gp 160 del 128-194	(1871)	TGATCGGCCTGCGCATCGTGTTCCGCGTGCTGAGCA----	
gp140TM	(2120)	TGATCGGCCTGCGCATCGTGTTCCGCGTGCTGAGCATCGT	
gp140	(2092)	-----	
gp140mut	(2092)	-----	
gp120	(1600)	-----	
Consensus	(2121)	TGATCGGCCTGCGCATCGTGTTCCGCGTGCTGAGCANNNN	

FIG. 66B-11

SUBSTITUTE SHEET (RULE 26)

108 / 131

		2161	2200
gp160	(2156)	-TCGTGAACCGCGTGC GCCAGGGCTACAGCCCCATCAGCC	
gp160 del V1	(2060)	-TCGTGAACCGCGTGC GCCAGGGCTACAGCCCCATCAGCC	
gp160 del V2	(2075)	-TCGTGAACCGCGTGC GCCAGGGCTACAGCCCCATCAGCC	
gp160 del V1-2	(1862)	-TCGTGAACCGCGTGC GCCAGGGCTACAGCCCCATCAGCC	
gp 160 del 128-194	(1907)	-TCGTGAACCGCGTGC GCCAGGGCTACAGCCCCATCAGCC	
gp140TM	(2160)	GTAAGATATCGGATCCTCTAGA-----	
gp140	(2092)	-TAAGATATCGGATCCTCTAGA-----	
gp140mut	(2092)	-TAAGATATCGGATCCTCTAGA-----	
gp120	(1600)	-----	
Consensus	(2161)	NTCGTGAACCGCGTGC GCCAGGGCTACAGCCCCATCAGCC	
		2201	2240
gp160	(2195)	TGCAGACCCGCCTGCCCCGCCAGCGCGGCCCCGACCGCCC	
gp160 del V1	(2099)	TGCAGACCCGCCTGCCCCGCCAGCGCGGCCCCGACCGCCC	
gp160 del V2	(2114)	TGCAGACCCGCCTGCCCCGCCAGCGCGGCCCCGACCGCCC	
gp160 del V1-2	(1901)	TGCAGACCCGCCTGCCCCGCCAGCGCGGCCCCGACCGCCC	
gp 160 del 128-194	(1946)	TGCAGACCCGCCTGCCCCGCCAGCGCGGCCCCGACCGCCC	
gp140TM	(2182)	-----	
gp140	(2113)	-----	
gp140mut	(2113)	-----	
gp120	(1600)	-----	
Consensus	(2201)	TGCAGACCCGCCTGCCCCGCCAGCGCGGCCCCGACCGCCC	
		2241	2280
gp160	(2235)	CGAGGGCATCGAGGAGGAGGGCGGCAGCGCGACCGCGAC	
gp160 del V1	(2139)	CGAGGGCATCGAGGAGGAGGGCGGCAGCGCGACCGCGAC	
gp160 del V2	(2154)	CGAGGGCATCGAGGAGGAGGGCGGCAGCGCGACCGCGAC	
gp160 del V1-2	(1941)	CGAGGGCATCGAGGAGGAGGGCGGCAGCGCGACCGCGAC	
gp 160 del 128-194	(1986)	CGAGGGCATCGAGGAGGAGGGCGGCAGCGCGACCGCGAC	
gp140TM	(2182)	-----	
gp140	(2113)	-----	
gp140mut	(2113)	-----	
gp120	(1600)	-----	
Consensus	(2241)	CGAGGGCATCGAGGAGGAGGGCGGCAGCGCGACCGCGAC	
		2281	2320
gp160	(2275)	CGCAGCAACCGCCTGGTGCACGGCCTGCTGGCCCTGATCT	
gp160 del V1	(2179)	CGCAGCAACCGCCTGGTGCACGGCCTGCTGGCCCTGATCT	
gp160 del V2	(2194)	CGCAGCAACCGCCTGGTGCACGGCCTGCTGGCCCTGATCT	
gp160 del V1-2	(1981)	CGCAGCAACCGCCTGGTGCACGGCCTGCTGGCCCTGATCT	
gp 160 del 128-194	(2026)	CGCAGCAACCGCCTGGTGCACGGCCTGCTGGCCCTGATCT	
gp140TM	(2182)	-----	
gp140	(2113)	-----	
gp140mut	(2113)	-----	
gp120	(1600)	-----	
Consensus	(2281)	CGCAGCAACCGCCTGGTGCACGGCCTGCTGGCCCTGATCT	
		2321	2360
gp160	(2315)	GGGACGACCTGCGCAGCCTGTGCCTGTTTCAGCTACCACCG	
gp160 del V1	(2219)	GGGACGACCTGCGCAGCCTGTGCCTGTTTCAGCTACCACCG	
gp160 del V2	(2234)	GGGACGACCTGCGCAGCCTGTGCCTGTTTCAGCTACCACCG	
gp160 del V1-2	(2021)	GGGACGACCTGCGCAGCCTGTGCCTGTTTCAGCTACCACCG	
gp 160 del 128-194	(2066)	GGGACGACCTGCGCAGCCTGTGCCTGTTTCAGCTACCACCG	
gp140TM	(2182)	-----	
gp140	(2113)	-----	
gp140mut	(2113)	-----	
gp120	(1600)	-----	
Consensus	(2321)	GGGACGACCTGCGCAGCCTGTGCCTGTTTCAGCTACCACCG	

FIG. 66B-12

SUBSTITUTE SHEET (RULE 26)

109/131		2361	2400
gp160	(2355)	CCTGCGCGACCTGCTGCTGATCGTGGCCCCGCATCGTGGAG	
gp160 del V1	(2259)	CCTGCGCGACCTGCTGCTGATCGTGGCCCCGCATCGTGGAG	
gp160 del V2	(2274)	CCTGCGCGACCTGCTGCTGATCGTGGCCCCGCATCGTGGAG	
gp160 del V1-2	(2061)	CCTGCGCGACCTGCTGCTGATCGTGGCCCCGCATCGTGGAG	
gp 160 del 128-194	(2106)	CCTGCGCGACCTGCTGCTGATCGTGGCCCCGCATCGTGGAG	
gp140TM	(2182)	-----	
gp140	(2113)	-----	
gp140mut	(2113)	-----	
gp120	(1600)	-----	
Consensus	(2361)	CCTGCGCGACCTGCTGCTGATCGTGGCCCCGCATCGTGGAG	
		2401	2440
gp160	(2395)	CTGCTGGGCCCCCGCGGCTGGGAGGCCCTGAAGTACTGGT	
gp160 del V1	(2299)	CTGCTGGGCCCCCGCGGCTGGGAGGCCCTGAAGTACTGGT	
gp160 del V2	(2314)	CTGCTGGGCCCCCGCGGCTGGGAGGCCCTGAAGTACTGGT	
gp160 del V1-2	(2101)	CTGCTGGGCCCCCGCGGCTGGGAGGCCCTGAAGTACTGGT	
gp 160 del 128-194	(2146)	CTGCTGGGCCCCCGCGGCTGGGAGGCCCTGAAGTACTGGT	
gp140TM	(2182)	-----	
gp140	(2113)	-----	
gp140mut	(2113)	-----	
gp120	(1600)	-----	
Consensus	(2401)	CTGCTGGGCCCCCGCGGCTGGGAGGCCCTGAAGTACTGGT	
		2441	2480
gp160	(2435)	GGAACCTGCTGCAGTACTGGAGCCAGGAGCTGAAGAGCAG	
gp160 del V1	(2339)	GGAACCTGCTGCAGTACTGGAGCCAGGAGCTGAAGAGCAG	
gp160 del V2	(2354)	GGAACCTGCTGCAGTACTGGAGCCAGGAGCTGAAGAGCAG	
gp160 del V1-2	(2141)	GGAACCTGCTGCAGTACTGGAGCCAGGAGCTGAAGAGCAG	
gp 160 del 128-194	(2186)	GGAACCTGCTGCAGTACTGGAGCCAGGAGCTGAAGAGCAG	
gp140TM	(2182)	-----	
gp140	(2113)	-----	
gp140mut	(2113)	-----	
gp120	(1600)	-----	
Consensus	(2441)	GGAACCTGCTGCAGTACTGGAGCCAGGAGCTGAAGAGCAG	
		2481	2520
gp160	(2475)	CGCCGTGAGCCTGTTCAACGCCACCGCCATCGCCGTGGCC	
gp160 del V1	(2379)	CGCCGTGAGCCTGTTCAACGCCACCGCCATCGCCGTGGCC	
gp160 del V2	(2394)	CGCCGTGAGCCTGTTCAACGCCACCGCCATCGCCGTGGCC	
gp160 del V1-2	(2181)	CGCCGTGAGCCTGTTCAACGCCACCGCCATCGCCGTGGCC	
gp 160 del 128-194	(2226)	CGCCGTGAGCCTGTTCAACGCCACCGCCATCGCCGTGGCC	
gp140TM	(2182)	-----	
gp140	(2113)	-----	
gp140mut	(2113)	-----	
gp120	(1600)	-----	
Consensus	(2481)	CGCCGTGAGCCTGTTCAACGCCACCGCCATCGCCGTGGCC	
		2521	2560
gp160	(2515)	GAGGGCACCGACCGCATCATCGAGATCGTGCAGCGCATCT	
gp160 del V1	(2419)	GAGGGCACCGACCGCATCATCGAGATCGTGCAGCGCATCT	
gp160 del V2	(2434)	GAGGGCACCGACCGCATCATCGAGATCGTGCAGCGCATCT	
gp160 del V1-2	(2221)	GAGGGCACCGACCGCATCATCGAGATCGTGCAGCGCATCT	
gp 160 del 128-194	(2266)	GAGGGCACCGACCGCATCATCGAGATCGTGCAGCGCATCT	
gp140TM	(2182)	-----	
gp140	(2113)	-----	
gp140mut	(2113)	-----	
gp120	(1600)	-----	
Consensus	(2521)	GAGGGCACCGACCGCATCATCGAGATCGTGCAGCGCATCT	

FIG. 66B-13

SUBSTITUTE SHEET (RULE 26)

		2561	2600
	gp160	(2555)	TCCGCGCCGTGATCCACATCCCCGCCGCATCCGCCAGGG
	gp160 del V1	(2459)	TCCGCGCCGTGATCCACATCCCCGCCGCATCCGCCAGGG
	gp160 del V2	(2474)	TCCGCGCCGTGATCCACATCCCCGCCGCATCCGCCAGGG
	gp160 del V1-2	(2261)	TCCGCGCCGTGATCCACATCCCCGCCGCATCCGCCAGGG
gp 160 del 128-194		(2306)	TCCGCGCCGTGATCCACATCCCCGCCGCATCCGCCAGGG
	gp140TM	(2182)	-----
	gp140	(2113)	-----
	gp140mut	(2113)	-----
	gp120	(1600)	-----
	Consensus	(2561)	TCCGCGCCGTGATCCACATCCCCGCCGCATCCGCCAGGG 2601
			2640
	gp160	(2595)	CCTGGAGCGCGCCCCTGCTGTAAGATATCGGATCCTCTAGA
	gp160 del V1	(2499)	CCTGGAGCGCGCCCCTGCTGTAAGATATCGGATCCTCTAGA
	gp160 del V2	(2514)	CCTGGAGCGCGCCCCTGCTGTAAGATATCGGATCCTCTAGA
	gp160 del V1-2	(2301)	CCTGGAGCGCGCCCCTGCTGTAAGATATCGGATCCTCTAGA
gp 160 del 128-194		(2346)	CCTGGAGCGCGCCCCTGCTGTAAGATATCGGATCCTCTAGA
	gp140TM	(2182)	-----
	gp140	(2113)	-----
	gp140mut	(2113)	-----
	gp120	(1600)	-----
	Consensus	(2601)	CCTGGAGCGCGCCCCTGCTGTAAGATATCGGATCCTCTAGA 2641
			2680
	gp160	(2635)	AAGCCATGGATATCGGATCCACTACGCGTTAGAGCTCGCT
	gp160 del V1	(2539)	-----
	gp160 del V2	(2554)	-----
	gp160 del V1-2	(2341)	-----
gp 160 del 128-194		(2386)	-----
	gp140TM	(2182)	-----
	gp140	(2113)	-----
	gp140mut	(2113)	-----
	gp120	(1600)	-----
	Consensus	(2641)	NNN 2681
			2681
	gp160	(2675)	GATCAGCT
	gp160 del V1	(2539)	-----
	gp160 del V2	(2554)	-----
	gp160 del V1-2	(2341)	-----
gp 160 del 128-194		(2386)	-----
	gp140TM	(2182)	-----
	gp140	(2113)	-----
	gp140mut	(2113)	-----
	gp120	(1600)	-----
	Consensus	(2681)	NNNNNNNN

SUBSTITUTE SHEET (RULE 26)

111 / 131

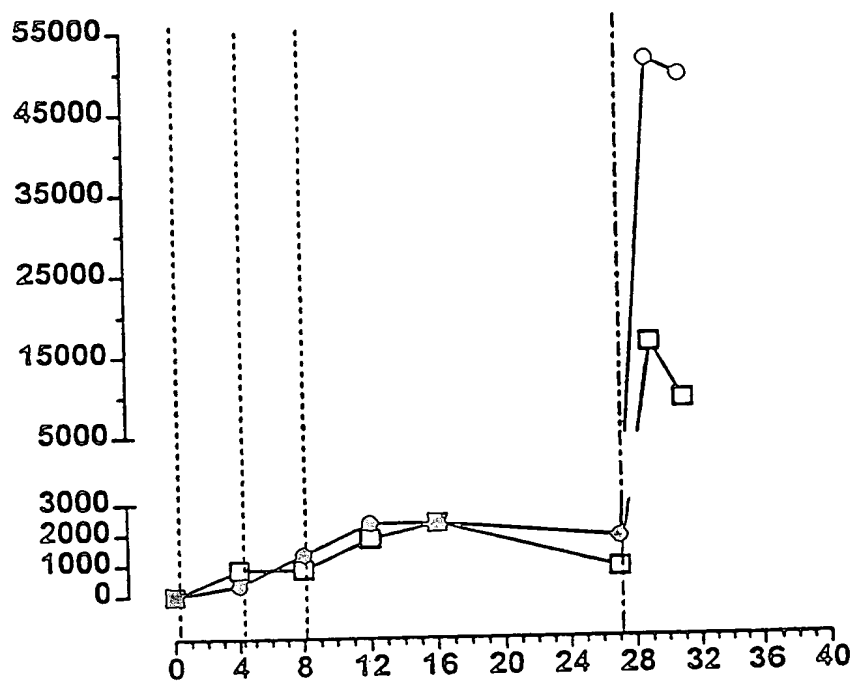


FIG. 67

112 / 131

HIV-1SF2 wt RT (PISPIET-->GIRKVL)

CCCATTAGTCCTATTGAAACTGTACCAGTAAAATTAAAGCCAGGAATGGATGGCCCCAAA
GTTAAGCAATGGCCATTGACAGAAGAAAAAATAAAAGCATTAGTAGAGATATGTACAGAA
ATGGAAAAGGAAGGGAAAATTTCAAAAATTGGGCCTGAAAATCCATACAATACTCCAGTA
TTTGCTATAAAGAAAAAGACAGTACTAAATGGAGAAAAGTAGTAGATTTTCAGAGAACTT
AATAAAAGAACTCAAGACTTCTGGGAAGTTCAGTTAGGAATACCACACCCCGCAGGGTTA
AAAAAGAAAAAATCAGTAACAGTATTGGATGTGGGTGATGCATACTTTTCAGTTCCCTTA
GATAAAGACTTTAGAAAGTATACTGCATTTACCATACCTAGTATAAACAATGAGACACCA
GGGATTAGATATCAGTACAATGTGCTGCCACAGGGATGGAAAGGATCACCAGCAATATTC
CAAAGTAGCATGACAAAAATCTTAGAGCCTTTTAGAAAACAGAATCCAGACATAGTTATC
TATCAAtacatggatgatTTGTATGTAGGATCTGACTTAGAAATAGGGCAGCATAGAACA
AAAATAGAGGAACTGAGACAGCATCTGTTGAGGTGGGGATTTACCACACCAGACAAAAAA
CATCAGAAAGAACCTCCATTCCCTTtggatgggttatGAACTCCATCCTGATAAATGGACA
GTACAGCCTATAATGCTGCCAGAAAAAGACAGCTGGACTGTCAATGACATACAGAAGTTA
GTGGGAAAATTGAATTGGGCAAGTCAGATTTATGCAGGGATTAAAGTAAAGCAGTTATGT
AAACTCCTTAGAGGAACCAAAGCACTAACAGAAGTAATACCACTAACAGAAGAAGCAGAG
CTAGAACTGGCAGAAAACAGGGAGATTCTAAAAGAACCAGTACATGAAGTATATTATGAC
CCATCAAAGACTTAGTAGCAGAAATACAGAAGCAGGGGCAAGGCCAATGGACATATCAA
ATTTATCAAGAGCCATTTAAAAATCTGAAAACAGGAAAGTATGCAAGGATGAGGGGTGCC
CACACTAATGATGTAAAACAGTTAACAGAGGCAGTGCAAAAAGTATCCACAGAAAGCATA
GTAATATGGGGAAAGATTCTAAATTTAAACTACCCATACAAAAGGAAACATGGGAAGCA
TGGTGGATGGAGTATTGGCAAGCTACCTGGATTCTGAGTGGGAGTTTGTCAATACCCCT
CCCTTAGTGAAATTATGGTACCAGTTAGAGAAAGAACCCATAGTAGGAGCAGAACTTTC
TATGTAGATGGGGCAGCTAATAGGGAGACTAAATTAGGAAAAGCAGGATATGTTACTGAC
AGAGGAAGACAAAAAGTTGTCTCCATAGCTGACACAACAAATCAGAAGACTGAATTACAA
GCAATTCATCTAGCTTTGCAGGATTCGGGATTAGAAGTAAACATAGTAACAGACTCACAA
TATGCATTAGGAATCATTCAAGCACAACCAGATAAGAGTGAATCAGAGTTAGTCAGTCAA
ATAATAGAGCAGTTAATAAAAAAGGAAAAGGTCTACCTGGCATGGGTACCAGCACACAAA
GGAATTGGAGGAAATGAACAAGTAGATAAATTAGTCAGTGCTGGAATCAGGAAAGTACTA

FIG. 68

(SEQ ID NO:77)

113 / 131

GagProtMod.SF2 (GP1)

GTCGACGCCACCATGGGCGCCCGCGCCAGCGTGCTGAGCGGCGGCGAGCTGGACAAGTGG
GAGAAGATCCGCCTGCGCCCCGGCGGCAAGAAGAAGTACAAGCTGAAGCACATCGTGTGG
GCCAGCCGCGAGCTGGAGCGCTTCGCCGTGAACCCCGGCCTGCTGGAGACCAGCGAGGGC
TGCCGCCAGATCCTGGGCCAGCTGCAGCCAGCCTGCAGACCGGCAGCGAGGAGCTGCGC
AGCCTGTACAACACCGTGGCCACCCTGTACTGCGTGCACCAGCGCATCGACGTCAAGGAC
ACCAAGGAGGCCCTGGAGAAGATCGAGGAGGAGCAGAACAAGTCCAAGAAGAAGGCCCAG
CAGGCCGCGCCGCGCCGCGGCACCGGCAACAGCAGCCAGGTGAGCCAGAACTACCCCATC
GTGCAGAACCTGCAGGGCCAGATGGTGCACCAGGCCATCAGCCCCGCGACCCTGAACGCC
TGGGTGAAGGTGGTGGAGGAGAAGGCCTTCAGCCCCGAGGTGATCCCCATGTTTCAGCGCC
CTGAGCGAGGGCGCCACCCCCCAGGACCTGAACACGATGTTGAACACCGTGGGCGGCCAC
CAGGCCGCCATGCAGATGCTGAAGGAGACCATCAACGAGGAGGCCGCGGAGTGGGACCGC
GTGCACCCCGTGCACGCGCGCCCCATCGCCCCCGGCCAGATGCGCGAGCCCCGCGGCAGC
GACATCGCCGGCACCACCAGCACCCCTGCAGGAGCAGATCGGCTGGATGACCAACAACCCC
CCCATCCCCGTGGGCGAGATCTACAAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTG
CGGATGTACAGCCCCACCAGCATCCTGGACATCCGCCAGGGCCCCAAGGAGCCCTTCCGC
GACTACGTGGACCGCTTCTACAAGACCCTGCGCGCTGAGCAGGCCAGCCAGGACGTGAAG
AACTGGATGACCGAGACCCTGCTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCCTG
AAGGCTCTCGGCCCCGCGGCCACCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGC
GGCCCCGGCCACAAGGCCCGCGTGCTGGCCGAGGCGATGAGCCAGGTGACGAACCCGGCG
ACCATCATGATGCAGCGCGGCAACTTCCGCAACCAGCGGAAGACCGTCAAGTGCTTCAAC
TGCGGCAAGGAGGGCCACACCGCCAGGAACTGCCGCGCCCCCGCAAGAAGGGCTGCTGG
CGCTGCGGCCGCGAAGGACACCAAATGAAAGATTGCACTGAGAGACAGGCTAATTTTTTA
GGGAAGATCTGGCCTTCCTACAAGGGAAGGCCAGGGAATTTTCTTCAGAGCAGACCAGAG
CCAACAGCCCCACCAGAAGAGAGCTTCAGGTTTGGGGAGGAGAAAACAACCTCCCTCTCAG
AAGCAGGAGCCGATAGACAAGGAACTGTATCCTTTAACTTCCCTCAGATCACTCTTTGGC
AACGACCCCTCGTCACAGTAAGGATCGGCGGCCAGCTCAAGGAGGCGCTGCTCGACACCG
GCGCCGACGACACCGTGCTGGAGGAGATGAACCTGCCCCGCAAGTGGAAAGCCCAAGATGA
TCGGCGGGGATCGGGGGCTTCATCAAGGTGCGGCAGTACGACCAGATCCCCGTGGAGATCT
GCGGCCACAAGGCCATCGGCACCGTGCTGGTGGGCCCCACCCCGTGAACATCATCGGCC
GCAACCTGCTGACCCAGATCGGCTGCACCCTGAACTTCCCCATCAGCCCCATCGAGACGG
TGCCCGTGAAGCTGAAGCCGGGGATGGACGGCCCCAAGGTCAAGCAGTGGCCCCCTGTAAG
AATTC

FIG. 69

(SEQ ID NO:78)

114 / 131

GagProtMod.SF2 (GP2)

GTTCGACGCCACCATGGGCGCCCGCGCCAGCGTGCTGAGCGGCGGCGAGCTGGACAAGTGG
GAGAAGATCCGCCTGCGCCCCGGCGGCAAGAAGAAGTACAAGCTGAAGCACATCGTGTGG
GCCAGCCGCGAGCTGGAGCGCTTCGCCGTGAACCCCGGCCTGCTGGAGACCAGCGAGGGC
TGCCGCCAGATCCTGGGCCAGCTGCAGCCCAGCCTGCAGACCGGCAGCGAGGAGCTGCGC
AGCCTGTACAACACCGTGGCCACCCTGTACTGCGTGCACCAGCGCATCGACGTCAAGGAC
ACCAAGGAGGCCCTGGAGAAGATCGAGGAGGAGCAGAACAAGTCCAAGAAGAAGGCCACG
CAGGCCGCGCCCGCCCGCCGGCACC GGCAACAGCAGCCAGGTGAGCCAGAACTACCCCATC
GTGCAGAACCTGCAGGGCCAGATGGTGCACCAGGCCATCAGCCCCCGCACCCCTGAACGCC
TGGGTGAAGGTGGTGGAGGAGAAGGCCTTCAGCCCCGAGGTGATCCCCATGTTTCAGCGCC
CTGAGCGAGGGCGCCACCCCCCAGGACCTGAACACGATGTTGAACACCGTGGGCGGCCAC
CAGGCCGCCATGCAGATGCTGAAGGAGACCATCAACGAGGAGGCCGCGGAGTGGGACCGC
GTGCACCCCGTGCACGCCGGCCCCATCGCCCCCGGCCAGATGCGCGAGCCCCGCGGCAGC
GACATCGCCGGCACCACCAGCACCTGCAGGAGCAGATCGGCTGGATGACCAACAACCCC
CCCATCCCCGTGGGCGAGATCTACAAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTG
CGGATGTACAGCCCCACCAGCATCCTGGACATCCGCCAGGGCCCCAAGGAGCCCTTCCGC
GACTACGTGGACCGCTTCTACAAGACCCTGCGCGCTGAGCAGGCCAGCCAGGACGTGAAG
AACTGGATGACCGAGACCCTGCTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCCTG
AAGGCTCTCGGCCCCGCGGCCACCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGCGC
GGCCCCGGCCACAAGGCCCGCGTGCTGGCCGAGGCGATGAGCCAGGTGACGAACCCGGCG
ACCATCATGATGCAGCGCGGCAACTTCCGCAACCAGCGGAAGACCGTCAAGTGCTTCAAC
TGCGGCAAGGAGGGCCACACCGCCAGGAACTGCCGCGCCCCCGCAAGAAGGGCTGCTGG
CGCTGCGGGCCGGAAGGACACCAAATGAAAGATTGCACTGAGAGACAGGCTAATTTTTTA
GGGAAGATCTGGCCTTCCTACAAGGGAAGGCCAGGGAATTTTCTTCAGAGCAGACCAGAG
CCAACAGCCCCACCAGAAGAGAGCTTCAGGTTTGGGGAGGAGAAAACAACTCCCTCTCAG
AAGCAGGAGCCGATAGACAAGGAACTGTATCCTTTAACTTCCCTCAGATCACTCTTTGGC
AACGACCCCTCGTCACAGTAAGGATCGGGGGGCAACTCAAGGAAGCGCTGCTCGATACAG
GAGCAGATGATACAGTATTAGAAGAAATGAATTTGCCAGGAAAATGGAAACCAAAAATGA
TAGGGGGGATCGGGGGCTTCATCAAGGTGAGGCAGTACGACCAGATACCTGTAGAAATCT
GTGGACATAAAGCTATAGGTACAGTATTAGTAGGACCTACACCTGTCAACATAATTGGAA
GAAATCTGTTGACCCAGATCGGCTGCACCTTGAACCTTCCCCATCAGCCCTATTGAGACGG
TGCCCGTGAAGTTGAAGCCGGGGATGGACGGCCCCAAGGTCAAGCAATGGCCATTGTAAG
AATTC

FIG. 70

(SEQ ID NO:79)

115 / 131

FS(+)_ProtInact_RTopt_YM

GCGGCCGCGAAGGACACCAAATGAAAGATTGCACTGAGAGACAGGCTAATTTTTTAGGGA
AGATCTGGCCTTCCTACAAGGGAAGGCCAGGGAATTTTCTTCAGAGCAGACCAGAGCCAA
CAGCCCCACCAGAAGAGAGCTTCAGGTTTGGGGAGGAGAAAACAACTCCCTCTCAGAAGC
AGGAGCCGATAGACAAGGAACTGTATCCTTTAACTTCCCTCAGATCACTCTTTGGCAACG
ACCCCTCGTCACAATAAGGATCGGGGGGCAACTCAAGGAAGCGCTGCTCGATACAGGAGC
AGATGATACAGTATTAGAAGAAATGAATTTGCCAGGAAAATGGAAACCAAAAATGATAGG
GGGGATCGGGGGCTTCATCAAGGTGAGGCAGTACGACCAGATACCTGTAGAAATCTGTGG
ACATAAAGCTATAGGTACAGTATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAAA
TCTGTTGACCCAGATCGGCTGCACCTTGAAGTTCCCCATCAGCCCTATTGAGACGGTGCC
CGTGAAGTTGAAGCCGGGGATGGACGGCCCCAAGGTCAAGCAATGGCCATTGACCGAGGA
GAAGATCAAGGCCCTGGTGGAGATCTGCACCGAGATGGAGAAGGAGGGCAAGATCAGCAA
GATCGGCCCCGAGAACCCCTACAACACCCCCGTGTTGCCATCAAGAAGAAGGACAGCAC
CAAGTGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGA
GGTGCAGCTGGGCATCCCCACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCT
GGACGTGGGCGACGCCTACTTCAGCGTGCCCCTGGACAAGGACTTCCGCAAGTACACCGC
CTTCACCATCCCCAGCATCAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCT
GCCCCAGGGCTGGAAGGGCAGCCCCGCCATCTTCAGAGCAGCATGACCAAGATCCTGGA
GCCCTTCCGCAAGCAGAACCCCGACATCGTGATCTACCAGGCCCCCCTGTACGTGGGCAG
CGACCTGGAGATCGGCCAGCACCCGACCAAGATCGAGGAGCTGCGCCAGCACCTGCTGCG
CTGGGGCTTCACCACCCCGACAAGAAGCACCAAGGAGCCCCCCTTCCTGTGGATGGG
CTACGAGCTGCACCCCGACAAGTGGAACCGTGAGCCCATCATGCTGCCCGAGAAGGACAG
CTGGACCGTGAAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTA
CGCCGGCATCAAGGTGAAGCAGCTGTGCAAGCTGCTGCGCGGCACCAAGGCCCTGACCGA
GGTGATCCCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGAA
GGAGCCCGTGACAGGTGTACTACGACCCCGCAAGGACCTGGTGGCCGAGATCCAGAA
GCAGGGCCAGGGCCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGAC
CGGCAAGTACGCCCCGATGCGCGGGCGCCACACCAACGACGTGAAGCAGCTGACCGAGGC
CGTGCAGAAGGTGAGCACCGAGAGCATCGTGATCTGGGGCAAGATCCCCAAGTTCAAGCT

FIG. 71A

(SEQ ID NO:80)

116 / 131

GCCCATCCAGAAGGAGACCTGGGAGGCCTGGTGGATGGAGTACTGGCAGGCCACCTGGAT
CCCCGAGTGGGAGTTCGTGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAA
GGAGCCCATCGTGGGCGCCGAGACCTTCTACGTGGACGGCGCCGCCAACCGCGAGACCAA
GCTGGGCAAGGCCGGCTACGTGACCGACCGGGGCCGGCAGAAGGTGGTGAGCATCGCCGA
CACCACCAACCAGAAGACCGAGCTGCAGGCCATCCACCTGGCCCTGCAGGACAGCGGCCT
GGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCGA
CAAGAGCGAGAGCGAGCTGGTGAGCCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGT
GTACCTGGCCTGGGTGCCCCGCCACAAGGGCATCGGCGGCAACGAGCAGGTGGACAAGCT
GGTGAGCGCCGGCATCCGCAAGGTGCTGTTCCCTGAACGGCATCGATGGCGGCATCGTGAT
CTACCAGTACATGGACGACCTGTACGTGGGCAGCGGCGGCCCTAGGATCGATTAAAAGCT
TCCCGGGGCTAGCACCGGTGAATTC

FIG. 71B

(SEQ ID NO:80)

117 / 131

FS(+)_ProtInact_RTopt_YMWM

GCGGCCGCGAAGGACACCAAATGAAAGATTGCACTGAGAGACAGGCTAATTTTTTAGGGA
AGATCTGGCCTTCCTACAAGGGAAGGCCAGGGAATTTTCTTCAGAGCAGACCAGAGCCAA
CAGCCCCACCAGAAGAGAGCTTCAGGTTTGGGGAGGAGAAAACAACTCCCTCTCAGAAGC
AGGAGCCGATAGACAAGGAACTGTATCCTTTAACTTCCCTCAGATCACTCTTTGGCAACG
ACCCCTCGTCACAATAAGGATCGGGGGGCAACTCAAGGAAGCGCTGCTCGATACAGGAGC
AGATGATACAGTATTAGAAGAAATGAATTTGCCAGGAAAATGGAAACCAAAAATGATAGG
GGGGATCGGGGGCTTCATCAAGGTGAGGCAGTACGACCAGATACCTGTAGAAATCTGTGG
ACATAAAGCTATAGGTACAGTATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAAA
TCTGTTGACCCAGATCGGCTGCACCTTGAACCTCCCCATCAGCCCTATTGAGACGGTGCC
CGTGAAGTTGAAGCCGGGGATGGACGGCCCCAAGGTCAAGCAATGGCCATTGACCGAGGA
GAAGATCAAGGCCCTGGTGGAGATCTGCACCGAGATGGAGAAGGAGGGCAAGATCAGCAA
GATCGGCCCCGAGAACCCTACAACACCCCGTGTTCCGCCATCAAGAAGAAGGACAGCAC
CAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGA
GGTGCAGCTGGGCATCCCCACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCT
GGACGTGGGCGACGCCTACTTCAGCGTGCCCCTGGACAAGGACTTCCGCAAGTACACCGC
CTTCACCATCCCCAGCATCAACAACGAGACCCCGGCATCCGCTACCAGTACAACGTGCT
GCCCCAGGGCTGGAAGGGCAGCCCCGCCATCTTCCAGAGCAGCATGACCAAGATCCTGGA
GCCCTTCCGCAAGCAGAACCCCGACATCGTGATCTACCAGGCCCCCCTGTACGTGGGCAG
CGACCTGGAGATCGGCCAGCACCGCACCAAGATCGAGGAGCTGCGCCAGCACCTGCTGCG
CTGGGGCTTCACCACCCCGACAAGAAGCACCAAGGAGCCCCCTTCCCTGCCCATCGA
GCTGCACCCCGACAAGTGGACCGTGCGAGCCCATCATGCTGCCCCGAGAAGGACAGCTGGAC
CGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACGCCGG
CATCAAGGTGAAGCAGCTGTGCAAGCTGCTGCGCGGCACCAAGGCCCTGACCGAGGTGAT
CCCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGAAGGAGCC
CGTGCACGAGGTGTACTACGACCCCGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGG
CCAGGGCCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAA
GTACGCCCCGATGCGCGGCGCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCA
GAAGGTGAGCACCGAGAGCATCGTGATCTGGGGCAAGATCCCCAAGTTCAAGCTGCCCAT

FIG. 72A

(SEQ ID NO:81)

SUBSTITUTE SHEET (RULE 26)

118 / 131

CCAGAAGGAGACCTGGGAGGCCTGGTGGATGGAGTACTGGCAGGCCACCTGGATCCCCGA
GTGGGAGTTCGTGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCC
CATCGTGGGCGCCGAGACCTTCTACGTGGACGGCGCCGCCAACCGCGAGACCAAGCTGGG
CAAGGCCGGCTACGTGACCGACCGGGGCGGCAGAAAGGTGGTGAGCATCGCCGACACCAC
CAACCAGAAGACCGAGCTGCAGGCCATCCACCTGGCCCTGCAGGACAGCGGCCTGGAGGT
GAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAG
CGAGAGCGAGCTGGTGAGCCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCT
GGCCTGGGTGCCCCGCCCAAGGGCATCGGCGGCAACGAGCAGGTGGACAAGCTGGTGAG
CGCCGGCATCCGCAAGGTGCTGTTCTGAACGGCATCGATGGCGGCATCGTGATCTACCA
GTACATGGACGACCTGTACGTGGGCAGCGGCGGCCCTAGGATCGATTAAAGCTTCCCCG
GGCTAGCACCGGTGAATTC

FIG. 72B

(SEQ ID NO:81)

119 / 131

FS(-)_ProtMod_RTopt_YM

GCGGCCGCGAAGGACACCAAATGAAAGATTGCACTGAGAGACAGGCTAATTTCTTCCGCC
AGGACCTGGCCTTCCTGCAGGGCAAGGCCCCGCGAGTTCAGCAGCGAGCAGACCCGCGCCA
ACAGCCCCACCCGCCGCGAGCTGCAGGTGTGGGGCGGCGAGAACAAACAGCCTGAGCGAGG
CCGGCGCCGACCGCCAGGGCACCGTGAGCTTCAACTTCCCCCAGATCACCTGTGGCAGC
GCCCCCTGGTGACCATCAGGATCGGCGGCCAGCTCAAGGAGGCGCTGCTCGACACCGGCG
CCGACGACACCGTGCTGGAGGAGATGAACCTGCCCCGCAAGTGGAAGCCCAAGATGATCG
GCGGGATCGGGGGCTTCATCAAGGTGCGGCAGTACGACCAGATCCCCGTGGAGATCTGCG
GCCACAAGGCCATCGGCACCGTGCTGGTGGGCCCCACCCCCGTGAACATCATCGGCCGCA
ACCTGCTGACCCAGATCGGCTGCACCCTGAACTTCCCCATCAGCCCCATCGAGACGGTG
CCGTGAAGCTGAAGCCGGGGATGGACGGCCCCAAGGTCAAGCAGTGGCCCCCTGACCGAGG
AGAAGATCAAGGCCCTGGTGGAGATCTGCACCGAGATGGAGAAGGAGGGCAAGATCAGCA
AGATCGGCCCCGAGAACCCCTACAACACCCCCGTGTTTCGCCATCAAGAAGAAGGACAGCA
CCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGG
AGGTGCAGCTGGGCATCCCCACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTG
TGGACGTGGGCGACGCCTACTTCAGCGTGCCCCCTGGACAAGGACTTCCGCAAGTACACCG
CCTTCACCATCCCCAGCATCAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGC
TGCCCCAGGGCTGGAAGGGCAGCCCCGCCATCTTCCAGAGCAGCATGACCAAGATCCTGG
AGCCCTTCCGCAAGCAGAACCCCGACATCGTGATCTACCAGGCCCCCCTGTACGTGGGCA
GCGACCTGGAGATCGGCCAGCACCGCACCAAGATCGAGGAGCTGCGCCAGCACCTGCTGC
GCTGGGGCTTCACCACCCCCGACAAGAAGCACCAGAAGGAGCCCCCCTTCTGTGGATGG
GCTACGAGCTGCACCCCGACAAGTGGACCGTGCGAGCCCATCATGCTGCCCCGAGAAGGACA
GCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCT
ACGCCGGCATCAAGGTGAAGCAGCTGTGCAAGCTGCTGCGCGGCACCAAGGCCCTGACCG
AGGTGATCCCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGA
AGGAGCCCGTGACGAGGTGTACTACGACCCAGCAAGGACCTGGTGGCCGAGATCCAGA
AGCAGGGCCAGGGCCAGTGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGA
CCGGCAAGTACGCCCGCATGCGCGGCGCCACACCAACGACGTGAAGCAGCTGACCGAGG
CCGTGCAGAAGGTGAGCACCGAGAGCATCGTGATCTGGGGCAAGATCCCCAAGTTCAAGC

FIG. 73A

(SEQ ID NO:82)

SUBSTITUTE SHEET (RULE 26)

120 / 131

TGCCCCATCCAGAAGGAGACCTGGGAGGCCTGGTGGATGGAGTACTGGCAGGCCACCTGGA
TCCCCGAGTGGGAGTTCGTGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGA
AGGAGCCCATCGTGGGCGCCGAGACCTTCTACGTGGACGGCGCCGCCAACCGCGAGACCA
AGCTGGGCAAGGCCGGCTACGTGACCGACCGGGGCGGCAGAAAGGTGGTGAGCATCGCCG
ACACCACCAACCAGAAGACCGAGCTGCAGGCCATCCACCTGGCCCTGCAGGACAGCGGCC
TGGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCCCG
ACAAGAGCGAGAGCGAGCTGGTGAGCCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGG
TGTACCTGGCCTGGGTGCCCCGCCACAAGGGCATCGGCGGCAACGAGCAGGTGGACAAGC
TGGTGAGCGCCGGCATCCGCAAGGTGCTGTTCTGAACGGCATCGATGGCGGCATCGTGA
TCTACCAGTACATGGACGACCTGTACGTGGGCAGCGGCGGCCCTAGGATCGATTAAAAGC
TTCCCGGGGCTAGCACCGGTGAATTC

FIG. 73B

(SEQ ID NO:82)

121 / 131

FS(-)_ProtMod_RTopt_YMWM

GCGGCCGCGAAGGACACCAAATGAAAGATTGCACTGAGAGACAGGCTAATTTCTTCCGCG
AGGACCTGGCCTTTCCTGCAGGGCAAGGCCCGCGAGTTCAGCAGCGAGCAGACCCGCGCCA
ACAGCCCCACCCGCCGCGAGCTGCAGGTGTGGGGCGGCGAGAACAACAGCCTGAGCGAGG
CCGGCGCCGACCGCCAGGGCACCGTGAGCTTCAACTTCCCCCAGATCACCTGTGGCAGC
GCCCCCTGGTGACCATCAGGATCGGCGGCCAGCTCAAGGAGGCGCTGCTCGACACCGGCG
CCGACGACACCGTGCTGGAGGAGATGAACCTGCCCCGGCAAGTGGAAGCCCAAGATGATCG
GCGGGATCGGGGGCTTCATCAAGGTGCGGCAGTACGACCAGATCCCCGTGGAGATCTGCG
GCCACAAGGCCATCGGCACCGTGCTGGTGGGCCCCACCCCGTGAAACATCATCGGCCGCA
ACCTGCTGACCCAGATCGGCTGCACCCTGAACTTCCCCATCAGCCCCATCGAGACGGTGC
CCGTGAAGCTGAAGCCGGGGATGGACGGCCCCAAGGTCAAGCAGTGGCCCCCTGACCGAGG
AGAAGATCAAGGCCCTGGTGGAGATCTGCACCGAGATGGAGAAGGAGGGCAAGATCAGCA
AGATCGGCCCCGAGAACCCCTACAACACCCCGTGTTCCGCATCAAGAAGAAGGACAGCA
CCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGG
AGGTGCAGCTGGGCATCCCCCACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGC
TGGACGTGGGCGACGCCTACTTCAGCGTGCCCCCTGGACAAGGACTTCCGCAAGTACACCG
CCTTCACCATCCCCAGCATCAACAACGAGACCCCGGCATCCGCTACCAGTACAACGTGC
TGCCCCAGGGCTGGAAGGGCAGCCCCGCCATCTTCCAGAGCAGCATGACCAAGATCCTGG
AGCCCTTCCGCAAGCAGAACCCCGACATCGTGATCTACCAGGCCCCCCTGTACGTGGGCA
GCGACCTGGAGATCGGCCAGCACCGCACCAAGATCGAGGAGCTGCGCCAGCACCTGCTGC
GCTGGGGCTTCACCACCCCGACAAGAAGCACCAAGGAGCCCCCCTTCTGCCCCATCG
AGCTGCACCCCGACAAGTGGACCGTGCGAGCCCATCATGCTGCCCCGAGAAGGACAGCTGGA
CCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACGCCG
GCATCAAGGTGAAGCAGCTGTGCAAGCTGCTGCGCGGCACCAAGGCCCTGACCGAGGTGA
TCCCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGAAGGAGC
CCGTGCACGAGGTGTACTACGACCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGG
GCCAGGGCCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCA
AGTACGCCCCGATGCGCGGCGCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGC
AGAAGGTGAGCACCGAGAGCATCGTGATCTGGGGCAAGATCCCCAAGTTCAAGCTGCCCA

FIG. 74A

(SEQ ID NO:83)

SUBSTITUTE SHEET (RULE 26)

122 / 131

TCCAGAAGGAGACCTGGGAGGCCTGGTGGATGGAGTACTGGCAGGCCACCTGGATCCCCG
AGTGGGAGTTCGTGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGC
CCATCGTGGGCGCCGAGACCTTCTACGTGGACGGCGCCGCCAACCGCGAGACCAAGCTGG
GCAAGGCCGGCTACGTGACCGACCGGGGGCCGGCAGAAGGTGGTGGAGCATCGCCGACACCA
CCAACCAGAAGACCGAGCTGCAGGCCATCCACCTGGCCCTGCAGGACAGCGGCCTGGAGG
TGAACATCCTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCCCGACAAGA
GCGAGAGCGAGCTGGTGAGCCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACC
TGGCCTGGGTGCCCCGCCACAAGGGCATCGGCGGCAACGAGCAGGTGGACAAGCTGGTGA
GCGCCGGCATCCGCAAGGTGCTGTTCCCTGAACGGCATCGATGGCGGCATCGTGATCTACC
AGTACATGGACGACCTGTACGTGGGCAGCGGCGGCCCTAGGATCGATTAAAAGCTTCCCG
GGGCTAGCACCGGTGAATTC

FIG. 74B

(SEQ ID NO:83)

123 / 131

FS(-)_ProtMod_RTopt(+)

GCGGCCGCGAAGGACACCAAATGAAAGATTGCACTGAGAGACAGGCTAATTTCTTCCGCG
AGGACCTGGCCTTTCCTGCAGGGCAAGGCCCGCGAGTTCAGCAGCGAGCAGACCCGCGCCA
ACAGCCCCACCCGCCGCGAGCTGCAGGTGTGGGGCGGCGAGAACAACAGCCTGAGCGAGG
CCGGCGCCGACCGCCAGGGCACCGTGAGCTTCAACTTCCCCCAGATCACCTGTGGCAGC
GCCCCCTGGTGACCATCAGGATCGGCGGCCAGCTCAAGGAGGCGCTGCTCGACACCGGCG
CCGACGACACCGTGCTGGAGGAGATGAACCTGCCCCGCAAGTGGAAGCCCAAGATGATCG
GCGGGATCGGGGGCTTCATCAAGGTGCGGCAGTACGACCAGATCCCCGTGGAGATCTGCG
GCCACAAGGCCATCGGCACCGTGCTGGTGGGCCCCACCCCGTGAACATCATCGGCCGCA
ACCTGCTGACCCAGATCGGCTGCACCTGAACTTCCCCATCAGCCCCATCGAGACGGTGC
CCGTGAAGCTGAAGCCGGGGATGGACGGCCCCAAGGTCAAGCAGTGGCCCCCTGACCGAGG
AGAAGATCAAGGCCCTGGTGGAGATCTGCACCGAGATGGAGAAGGAGGGCAAGATCAGCA
AGATCGGCCCCGAGAACCCCTACAACACCCCGTGTTCGCCATCAAGAAGAAGGACAGCA
CCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGG
AGGTGCAGCTGGGCATCCCCACCCCGCCGCTGAAGAAGAAGAAGAGCGTGACCGTGC
TGGACGTGGGCGACGCCTACTTCAGCGTGCCCCCTGGACAAGGACTTCCGCAAGTACACCG
CCTTCACCATCCCCAGCATCAACAACGAGACCCCGGCATCCGCTACCAGTACAACGTGC
TGCCCCAGGGCTGGAAGGGCAGCCCCGCCATCTTCCAGAGCAGCATGACCAAGATCCTGG
AGCCCTTCCGCAAGCAGAACCCCGACATCGTGATCTACCAGTACATGGACGACCTGTACG
TGGGCAGCGACCTGGAGATCGGCCAGCACCGCACCAAGATCGAGGAGCTGCGCCAGCACC
TGCTGCGCTGGGGCTTACCACCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCTGT
GGATGGGCTACGAGCTGCACCCCGACAAGTGGACCGTGCGAGCCCATCATGCTGCCCCGAGA
AGGACAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCC
AGATCTACGCCGGCATCAAGGTGAAGCAGCTGTGCAAGCTGCTGCGCGGCACCAAGGCCC
TGACCGAGGTGATCCCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGA
TCCTGAAGGAGCCCGTGACGAGGTGTACTACGACCCCGACAAGGACCTGGTGGCCGAGA
TCCAGAAGCAGGGCCAGGGCCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACC
TGAAGACCGGCAAGTACGCCCCGATGCGCGGCGCCACACCAACGACGTGAAGCAGCTGA
CCGAGGCCGTGCAGAAGGTGAGCACCGAGAGCATCGTGATCTGGGGCAAGATCCCCAAGT
TCAAGCTGCCCATCCAGAAGGAGACCTGGGAGGCCTGGTGGATGGAGTACTGGCAGGCCA
CCTGGATCCCCGAGTGGGAGTTCGTGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGC
TGGAGAAGGAGCCCATCGTGGGCGCCGAGACCTTCTACGTGGACGGCGCCGCCAACC

FIG. 75A
(SEQ ID NO:84)

124/131

AGACCAAGCTGGGCAAGGCCGGCTACGTGACCGACCGGGGCCGGCAGAAGGTGGTGAGCA
TCGCCGACACCACCAACCAGAAGACCGAGCTGCAGGCCATCCACCTGGCCCTGCAGGACA
GCGGCCTGGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCC
AGCCCGACAAGAGCGAGAGCGAGCTGGTGAGCCAGATCATCGAGCAGCTGATCAAGAAGG
AGAAGGTGTACCTGGCCTGGGTGCCCCGCCCAAGGGCATCGGCGGCAACGAGCAGGTGG
ACAAGCTGGTGAGCGCCGGCATCCGCAAGGTGCTGTTCTGAACGGCATCGATGGCGGCA
TCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGGCGGCCCTAGGATCGATT
AAAAGCTTCCCGGGGCTAGCACCGGTGAATTC

FIG. 75B
(SEQ ID NO:84)

125 / 131

Tat_wt_SF162 (wildtype)

ATGGAGCCAGTAGATCCTAGATTAGAGCCCTGGAAGCATCCAGGAAGTCAGCCTAAGA
CTGCTTGTACAAATTGCTATTGTAAAAAGTGTTGCTTTCATTGCCAAGTTTGTTCATAAC
AAAAGGCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGACAGCGACGAAGAGCTCCT
CCAGACAGTGAGGTTTCATCAAGTTTCTCTACCAAAGCAACCCGCTTCCCAGCCCCAAGG
GGACCCGACAGGCCCGAAGGAATCGAAGAAGAAGGTGGAGAGAGAGACAGAGACAGA
TCCAGTCCATTAG

FIG. 76

(SEQ ID NO:85)

Tat_SF162

MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKGLGISYGRKKRRQRRRAPDSE
VHQVSLPKQPASQPQGDPTGPKESKKKVERETETDPVH

FIG. 77

(SEQ ID NO:86)

Tat_SF162_opt

ATGGAGCCCGTGGACCCCCGCCTGGAGCCCTGGAAGCACCCCGGCAGCCAGCCCAAGAC
CGCCTGCACCAACTGCTACTGCAAGAAGTGCTGCTTCCACTGCCAGGTGTGCTTCATCACC
AAGGGCCTGGGCATCAGCTACGGCCGCAAGAAGCGCCGCCAGCGCCGCCGCCGCCCCCCC
CGACAGCGAGGTGCACCAGGTGAGCCTGCCCAAGCAGCCCGCCAGCCAGCCCCAGGGCG
ACCCACCCGGCCCCAAGGAGAGCAAGAAGAAGGTGGAGCGCGAGACCGAGACCGACCCC
GTGCACTAG

FIG. 78

(SEQ ID NO:87)

Tat_Cys22_SF162_opt

ATGGAGCCCGTGGACCCCCGCCTGGAGCCCTGGAAGCACCCCGGCAGCCAGCCCAAGAC
CGCCGACCAACTGCTACTGCAAGAAGTGCTGCTTCCACTGCCAGGTGTGCTTCATCACC
AGGGCCTGGGCATCAGCTACGGCCGCAAGAAGCGCCGCCAGCGCCGCCGCCGCCCCCCCC
GACAGCGAGGTGCACCAGGTGAGCCTGCCCAAGCAGCCCGCCAGCCAGCCCCAGGGCGA
CCCCACCCGGCCCCAAGGAGAGCAAGAAGAAGGTGGAGCGCGAGACCGAGACCGACCCCG
TGCACTAG

FIG. 79

(SEQ ID NO:88)

126 / 131

Alignment GagMod vs GP1_GP2

		10	20	30	40	50	60	76	Section 1
GagMod.SF2	(1)	1							
GagProtMod.SF2 (GP1)	(1)	ATGGGCGCCCGCCAGCGT	GCTGAGCGGCGGCGAGCT	GGACAAAGTGGGAGAAGAT	CCGCCTGCGCCCCCGGGGCA				
GagProtMod.SF2 (GP2)	(1)	ATGGGCGCCCGCCAGCGT	GCTGAGCGGCGGCGAGCT	GGACAAAGTGGGAGAAGAT	CCGCCTGCGCCCCCGGGGCA				
Consensus	(1)	ATGGGCGCCCGCCAGCGT	GCTGAGCGGCGGCGGAGCT	GGACAAAGTGGGAGAAGAT	CCGCCTGCGCCCCCGGGGCA				
									Section 2
GagMod.SF2	(77)	77	90	100	110	120	130	140	152
GagProtMod.SF2 (GP1)	(77)	AGAAAGTACAAGCTGAAG	CACATCGTGTGGGCCAGCG	GAGCTGGAGCGCTT	CGCCGTGAACCCCGGCCTGCT				
GagProtMod.SF2 (GP2)	(77)	AGAAAGTACAAGCTGAAG	CACATCGTGTGGGCCAGCG	GAGCTGGAGCGCTT	CGCCGTGAACCCCGGCCTGCT				
Consensus	(77)	AGAAAGTACAAGCTGAAG	CACATCGTGTGGGCCAGCG	GAGCTGGAGCGCTT	CGCCGTGAACCCCGGCCTGCT				
									Section 3
GagMod.SF2	(153)	153	160	170	180	190	200	210	228
GagProtMod.SF2 (GP1)	(153)	GGAGACCGGAGGGGTGCC	GGCCAGATCCTGGGCCAGCT	GCAGCCCGAGCCGCGAG	CGGCGGAGAGGAGCTGCGC				
GagProtMod.SF2 (GP2)	(153)	GGAGACCGGAGGGGTGCC	GGCCAGATCCTGGGCCAGCT	GCAGCCCGAGCCGCGAG	CGGCGGAGAGGAGCTGCGC				
Consensus	(153)	GGAGACCGGAGGGGTGCC	GGCCAGATCCTGGGCCAGCT	GCAGCCCGAGCCGCGAG	CGGCGGAGAGGAGCTGCGC				
									Section 4
GagMod.SF2	(229)	229	240	250	260	270	280	290	304
GagProtMod.SF2 (GP1)	(229)	AGCCTGTACAACACCGTG	GCCACCCCTGTACTGCGT	GCACCGCATCGACGT	CAAGGACACCAAGAGGCCCTGG				
GagProtMod.SF2 (GP2)	(229)	AGCCTGTACAACACCGTG	GCCACCCCTGTACTGCGT	GCACCGCATCGACGT	CAAGGACACCAAGAGGCCCTGG				
Consensus	(229)	AGCCTGTACAACACCGTG	GCCACCCCTGTACTGCGT	GCACCGCATCGACGT	CAAGGACACCAAGAGGCCCTGG				
									Section 5
GagMod.SF2	(305)	305	310	320	330	340	350	360	370
GagProtMod.SF2 (GP1)	(305)	AGAAGATCGAGGAGGAGC	AGAAACAAGTCCAAGAAG	AGGCCCCAGCAGGCGCG	CGCCCGCGCGGACCGGCAACAG				
GagProtMod.SF2 (GP2)	(305)	AGAAGATCGAGGAGGAGC	AGAAACAAGTCCAAGAAG	AGGCCCCAGCAGGCGCG	CGCCCGCGGACCGGCAACAG				
Consensus	(305)	AGAAGATCGAGGAGGAGC	AGAAACAAGTCCAAGAAG	AGGCCCCAGCAGGCGCG	CGCCCGCGGACCGGCAACAG				

FIG. 80A

127 / 131

Alignment GagMod vs GP1_GP2

	381	390	400	410	420	430	440	Section 6
GagMod.SF2	(381)	381	390	400	410	420	430	456
GagProtMod.SF2 (GP1)	(381)	CAGCCAGGTGAGCCAGAACTACCCCATCGTGAGAACTGTCAGGGCCAGATGGTGACACAGGCCCATCAGCCCCCGC						
GagProtMod.SF2 (GP2)	(381)	CAGCCAGGTGAGCCAGAACTACCCCATCGTGAGAACTGTCAGGGCCAGATGGTGACACAGGCCCATCAGCCCCCGC						
Consensus	(381)	CAGCCAGGTGAGCCAGAACTACCCCATCGTGAGAACTGTCAGGGCCAGATGGTGACACAGGCCCATCAGCCCCCGC						
	(457)	457	470	480	490	500	510	Section 7
GagMod.SF2	(457)	ACCCTGAACGCCTGGTGAAGTGGTGGAGGAGAAAGCCTTCAGCCCCGAGGTGATCCCCATGTTACAGCGCCCTGA						532
GagProtMod.SF2 (GP1)	(457)	ACCCTGAACGCCTGGTGAAGTGGTGGAGGAGAAAGCCTTCAGCCCCGAGGTGATCCCCATGTTACAGCGCCCTGA						
GagProtMod.SF2 (GP2)	(457)	ACCCTGAACGCCTGGTGAAGTGGTGGAGGAGAAAGCCTTCAGCCCCGAGGTGATCCCCATGTTACAGCGCCCTGA						
Consensus	(457)	ACCCTGAACGCCTGGTGAAGTGGTGGAGGAGAAAGCCTTCAGCCCCGAGGTGATCCCCATGTTACAGCGCCCTGA						
	(533)	533	540	550	560	570	580	Section 8
GagMod.SF2	(533)	GCGAGGGCGCCACCCCGAGGACCTGAACACGATGTTGAACACCGTGGCGGCCACAGCGGCCCATGCAGATGCT						608
GagProtMod.SF2 (GP1)	(533)	GCGAGGGCGCCACCCCGAGGACCTGAACACGATGTTGAACACCGTGGCGGCCACAGCGGCCCATGCAGATGCT						
GagProtMod.SF2 (GP2)	(533)	GCGAGGGCGCCACCCCGAGGACCTGAACACGATGTTGAACACCGTGGCGGCCACAGCGGCCCATGCAGATGCT						
Consensus	(533)	GCGAGGGCGCCACCCCGAGGACCTGAACACGATGTTGAACACCGTGGCGGCCACAGCGGCCCATGCAGATGCT						
	(609)	609	620	630	640	650	660	Section 9
GagMod.SF2	(609)	GAAGGAGACCATCAACGAGGAGGCGCCGAGTGGGACCGCGTGACACCCCGTGACGCGCGGCCCATCGCCCCCGGC						684
GagProtMod.SF2 (GP1)	(609)	GAAGGAGACCATCAACGAGGAGGCGCCGAGTGGGACCGCGTGACACCCCGTGACGCGCGGCCCATCGCCCCCGGC						
GagProtMod.SF2 (GP2)	(609)	GAAGGAGACCATCAACGAGGAGGCGCCGAGTGGGACCGCGTGACACCCCGTGACGCGCGGCCCATCGCCCCCGGC						
Consensus	(609)	GAAGGAGACCATCAACGAGGAGGCGCCGAGTGGGACCGCGTGACACCCCGTGACGCGCGGCCCATCGCCCCCGGC						
	(685)	685	690	700	710	720	730	Section 10
GagMod.SF2	(685)	CAGATGCGCGAGCCCCGGCGGACGACATGCGCGGACCAACAGCACCCCTGCAGGAGCAGATCGGCTGGATGACCA						760
GagProtMod.SF2 (GP1)	(685)	CAGATGCGCGAGCCCCGGCGGACGACATGCGCGGACCAACAGCACCCCTGCAGGAGCAGATCGGCTGGATGACCA						
GagProtMod.SF2 (GP2)	(685)	CAGATGCGCGAGCCCCGGCGGACGACATGCGCGGACCAACAGCACCCCTGCAGGAGCAGATCGGCTGGATGACCA						
Consensus	(685)	CAGATGCGCGAGCCCCGGCGGACGACATGCGCGGACCAACAGCACCCCTGCAGGAGCAGATCGGCTGGATGACCA						

FIG. 80B

Alignment GagMod vs GP1_GP2

	(761)	761	770	780	790	800	810	820	836	Section 11
GagMod.SF2	(761)	ACAA	CCCCC	CCAT	CCCCG	TGGCGAGATCTACA	GGGTGGATCATCCTGGGCCTGAACA	AGATCGTGGCGATGTA		
GagProtMod.SF2(GP1)	(761)	ACAA	CCCCC	CCAT	CCCCG	TGGCGAGATCTACA	GGGTGGATCATCCTGGGCCTGAACA	AGATCGTGGCGATGTA		
GagProtMod.SF2(GP2)	(761)	ACAA	CCCCC	CCAT	CCCCG	TGGCGAGATCTACA	GGGTGGATCATCCTGGGCCTGAACA	AGATCGTGGCGATGTA		
Consensus	(761)	ACAA	CCCCC	CCAT	CCCCG	TGGCGAGATCTACA	GGGTGGATCATCCTGGGCCTGAACA	AGATCGTGGCGATGTA		Section 12
	(837)	837	850	860	870	880	890	900	912	
GagMod.SF2	(837)	CAGC	CCCACC	CAGCATCCTGG	ACATCCGCCAGG	CCCCCAAGGAGCCCTTC	CGCGACTACGTGG	ACCGCTTCTACAAG		
GagProtMod.SF2(GP1)	(837)	CAGC	CCCACC	CAGCATCCTGG	ACATCCGCCAGG	CCCCCAAGGAGCCCTTC	CGCGACTACGTGG	ACCGCTTCTACAAG		
GagProtMod.SF2(GP2)	(837)	CAGC	CCCACC	CAGCATCCTGG	ACATCCGCCAGG	CCCCCAAGGAGCCCTTC	CGCGACTACGTGG	ACCGCTTCTACAAG		
Consensus	(837)	CAGC	CCCACC	CAGCATCCTGG	ACATCCGCCAGG	CCCCCAAGGAGCCCTTC	CGCGACTACGTGG	ACCGCTTCTACAAG		Section 13
	(913)	913	920	930	940	950	960	970	988	
GagMod.SF2	(913)	ACCC	TGCGCGCTGAG	CAGGCCAGCCAGG	ACGTGAAGA	ACTGGATGACCGAG	ACCCCTGCTGGT	GCAGAACGCCAACC		
GagProtMod.SF2(GP1)	(913)	ACCC	TGCGCGCTGAG	CAGGCCAGCCAGG	ACGTGAAGA	ACTGGATGACCGAG	ACCCCTGCTGGT	GCAGAACGCCAACC		
GagProtMod.SF2(GP2)	(913)	ACCC	TGCGCGCTGAG	CAGGCCAGCCAGG	ACGTGAAGA	ACTGGATGACCGAG	ACCCCTGCTGGT	GCAGAACGCCAACC		
Consensus	(913)	ACCC	TGCGCGCTGAG	CAGGCCAGCCAGG	ACGTGAAGA	ACTGGATGACCGAG	ACCCCTGCTGGT	GCAGAACGCCAACC		Section 14
	(989)	989	1000	1010	1020	1030	1040	1050	1064	
GagMod.SF2	(989)	CCGACTGCA	AAGACCATCCTGA	AGGCTCTCGG	CCCCCGCGGCCAC	CCCTTGAGGAGATGATAC	CGCCTGCCAGGCGGT			
GagProtMod.SF2(GP1)	(989)	CCGACTGCA	AAGACCATCCTGA	AGGCTCTCGG	CCCCCGCGGCCAC	CCCTTGAGGAGATGATAC	CGCCTGCCAGGCGGT			
GagProtMod.SF2(GP2)	(989)	CCGACTGCA	AAGACCATCCTGA	AGGCTCTCGG	CCCCCGCGGCCAC	CCCTTGAGGAGATGATAC	CGCCTGCCAGGCGGT			
Consensus	(989)	CCGACTGCA	AAGACCATCCTGA	AGGCTCTCGG	CCCCCGCGGCCAC	CCCTTGAGGAGATGATAC	CGCCTGCCAGGCGGT			Section 15
	(1065)	1065	1070	1080	1090	1100	1110	1120	1130	1140
GagMod.SF2	(1065)	GGGCGG	CCCCCGGCACAA	GGCCGCGTGTGG	CCGAGGCGGATGAG	CCAGGTGACGA	ACCCGGCGCACCATCAT	GATG		
GagProtMod.SF2(GP1)	(1065)	GGGCGG	CCCCCGGCACAA	GGCCGCGTGTGG	CCGAGGCGGATGAG	CCAGGTGACGA	ACCCGGCGCACCATCAT	GATG		
GagProtMod.SF2(GP2)	(1065)	GGGCGG	CCCCCGGCACAA	GGCCGCGTGTGG	CCGAGGCGGATGAG	CCAGGTGACGA	ACCCGGCGCACCATCAT	GATG		
Consensus	(1065)	GGGCGG	CCCCCGGCACAA	GGCCGCGTGTGG	CCGAGGCGGATGAG	CCAGGTGACGA	ACCCGGCGCACCATCAT	GATG		

FIG. 80C

129/131

Alignment GagMod vs GP1_GP2

	1141	1150	1160	1170	1180	1190	1200	1216	Section 16
GagMod.SF2 (1141)	(1141)								
GagProtMod.SF2 (GP1) (1141)									
GagProtMod.SF2 (GP2) (1141)									
Consensus (1141)									
	1217	1230	1240	1250	1260	1270	1280	1292	Section 17
GagMod.SF2 (1217)	(1217)								
GagProtMod.SF2 (GP1) (1217)									
GagProtMod.SF2 (GP2) (1217)									
Consensus (1217)									
	1293	1300	1310	1320	1330	1340	1350	1368	Section 18
GagMod.SF2 (1293)	(1293)								
GagProtMod.SF2 (GP1) (1293)									
GagProtMod.SF2 (GP2) (1293)									
Consensus (1293)									
	1369	1380	1390	1400	1410	1420	1430	1444	Section 19
GagMod.SF2 (1369)	(1369)								
GagProtMod.SF2 (GP1) (1369)									
GagProtMod.SF2 (GP2) (1369)									
Consensus (1369)									
	1445	1450	1460	1470	1480	1490	1500	1510	Section 20
GagMod.SF2 (1445)	(1445)								
GagProtMod.SF2 (GP1) (1445)									
GagProtMod.SF2 (GP2) (1445)									
Consensus (1445)									

FIG. 80D

130/ 131

Alignment GagMod vs GP1_GP2

	1521	1530	1540	1550	1560	1570	1580	1596	Section 21
GagMod.SF2(1510)	(1521)	1521	1530	1540	1550	1560	1570	1580	1596
GagProtMod.SF2(GP1)(1521)									
GagProtMod.SF2(GP2)(1521)									
Consensus(1521)									
GagMod.SF2(1510)	(1597)	1597	1610	1620	1630	1640	1650	1660	1672
GagProtMod.SF2(GP1)(1597)									
GagProtMod.SF2(GP2)(1597)									
Consensus(1597)									
GagMod.SF2(1510)	(1673)	1673	1680	1690	1700	1710	1720	1730	1748
GagProtMod.SF2(GP1)(1673)									
GagProtMod.SF2(GP2)(1673)									
Consensus(1673)									
GagMod.SF2(1510)	(1749)	1749	1760	1770	1780	1790	1800	1810	1824
GagProtMod.SF2(GP1)(1749)									
GagProtMod.SF2(GP2)(1749)									
Consensus(1749)									
GagMod.SF2(1510)	(1825)	1825	1830	1847					
GagProtMod.SF2(GP1)(1825)									
GagProtMod.SF2(GP2)(1825)									
Consensus(1825)									

FIG. 80E

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131/ 131

TataminoSF162.opt

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FIG. 81
(SEQ ID NO:89)

Tat_Cys22_SF162

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FIG. 82
(SEQ ID NO:90)

SEQUENCE LISTING

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<120> IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
OF VIRUS-LIKE PARTICLES

<130> 1621.100

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aagataatag tgacataaaa gtagtgccaa gaagaaaaag aaaaatcatt agggattatg 4260
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```

<210> 4

<211> 1515

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
HIV-Gag

<400> 4

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cgcgagctgg agcgcttcgc cgtgaacccc ggcctgctgg agaccagcga gggctgccgc 180
cagatcctgg gccagctgca gccagcctg cagaccggca gcgaggagct gcgcagcctg 240
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gccgccgcgc ccggcaccgg caacagcagc caggtgagcc agaactacc catcgtgcag 420
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aaggtgggtg aggagaaggc cttcagcccc gaggtgatcc ccatgttcag cgccctgagc 540
gagggcgcca cccccagga cctgaacacg atgttgaaca ccgtgggcgg ccaccaggcc 600
gccatgcaga tgctgaagga gaccatcaac gaggaggccg ccgagtggga ccgcgtgcac 660
cccgtgcacg ccggccccat cgcccccggc cagatgcgcg agccccgcgg cagcgacatc 720
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gcccccccg aggagagctt ccgcttcggc gaggagaaga ccaccccgag ccagaagcag 1440
gagcccatcg acaaggagct gtacccctg accagcctgc gcagcctgtt cggcaacgac 1500
cccagcagcc agtaa

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<210> 5

<211> 1853

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
HIV-Gag-protease

<400> 5

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cgcgagctgg agcgcttcgc cgtgaacccc ggcctgctgg agaccagcga gggctgccgc 180
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aacctgcagg gccagatggg gcaccaggcc atcagcccc gcaccctgaa cgcctgggtg 480
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acaaggccat cggcaccgtg ctggtggggc ccacccccgt gaacatcatc ggccgcaacc 1740
tgctgaccca gatcggctgc accctgaact tccccatcag ccccatcgag acggtgcccc 1800
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```

<210> 6

<211> 4319

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
HIV-Gag-polymerase

<400> 6

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cgcgagctgg agcgcttcgc cgtgaacccc ggctgctgg agaccagcga gggctgccgc 180
cagatcctgg gccagctgca gccagcctg cagaccggca gcgaggagct gcgcagcctg 240
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gaggccctgg agaagatcga ggaggagcag aacaagtcca agaagaaggc ccagcaggcc 360
gccgcccggc cgggcaccgg caacagcagc caggtgagcc agaactacct catcgtgcag 420
aacctgcagg gccagatggg gcaccaggcc atcagcccc gcaccctgaa cgcctgggtg 480
aaggtgggtg aggagaaggc cttcagcccc gaggtgatcc ccatgttcag cgccctgagc 540
gagggcgcca cccccaggga cctgaacacg atgttgaaaca ccgtgggcgg ccaccaggcc 600
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cccagggtg gaagggcagc cccgccatct tccagagcag catgaccaag atcctggagc 2280
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tgatccagga caacagcgac atcaagggtg tgccccgcg caaggccaag atcatccgcg 4260
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```

<210> 7

<211> 2031

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
HIV-Gag/HCV-core fusion polypeptide

<400> 7

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atccgcctgc gccccggcgg caagaagaag tacaagctga agcacatcgt gtggggccagc 120
cgcgagctgg agcgtctcgc cgtgaacccc ggcctgctgg agaccagcga gggctgccgc 180
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gccgcccggc ccggcaccgg caacagcagc caggtgagcc agaactacc catcgtgcag 420
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gccggcacca ccagcaccct gcaggagcag atcggctgga tgaccaacaa ccccccatc 780
cccgtgggcg agatctacaa gcggtggatc atcctgggcc tgaacaagat cgtgcggatg 840
tacagcccca ccagcatcct ggacatccgc cagggcccca aggagccctt ccgcgactac 900

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ccgctcgtcg gcgccccctt tggaggcgct gccagggccc tggcgcatgg cgtccgggtt 1980
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```

<210> 8

<211> 2025

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
HIV-Gag/HCV-Core fusion polypeptide

<400> 8

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ttaaggccag ggggaaagaa aaaatataag ttaaaacata tagtatgggc aagcaggag 120
ctagaacgat tcgcagtcaa tcctggcctg ttagaaacat cagaaggctg cagacaaata 180
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caaatgttaa aagagactat caatgaggaa gctgcagaat gggatagagt gcatccagt 660
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```

<210> 9
 <211> 1268
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic Gag
 common region

```

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<210> 10
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: HIV-Gag
 peptide p7G

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<400> 10
Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
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Glu Ala Ala Glu
          20

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<210> 11
 <211> 30
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer GAG5

<400> 11

aagaattcca tgggtgag agcgctcgta

30

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer
p55-SAL3

<400> 12

attcgatgac tggatgaggg ggatggtgac

30

<210> 13

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer
CORESAL5

<400> 13

atttgatgac gaatcctaaa cctcaaagaa aaac

34

<210> 14

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer 173CORE

<400> 14

tattggatcc taagagcaac caggaagggt c

31

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer MS65

<400> 15

cgaccatcat ggatgcagcg c

21

<210> 16

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer MS66

<400> 16

aggattcgtc gagtcgctgc tggggtcgtt

30

<210> 17

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer XPANXNF

<400> 17

gcacgtgggc ccggcgctc tagagc

26

<210> 18

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer XPANXNR

<400> 18

gctctagagg cgccgggccc acgtgc

26

<210> 19

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HIV p55 Gag
Major Homology Region

<400> 19

Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg
1 5 10 15Phe Tyr Lys Thr
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<210> 20

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic p55
Gag Major Homology Region

<400> 20

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<210> 21

<211> 15

<212> PRT
<213> Human immunodeficiency virus

<400> 21
Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg
1 5 10 15

<210> 22
<211> 5
<212> PRT
<213> Human immunodeficiency virus

<400> 22
Lys Ala Lys Arg Arg
1 5

<210> 23
<211> 4
<212> PRT
<213> Human immunodeficiency virus

<400> 23
Arg Glu Lys Arg
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<210> 24
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: aa of
mut7.SF162 cleavage site

<400> 24
Ala Pro Thr Lys Ala Ile Ser Ser Val Val Gln Ser Glu Lys Ser
1 5 10 15

<210> 25
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: aa of
mut8.SF162 cleavage site

<400> 25
Ala Pro Thr Ile Ala Ile Ser Ser Val Val Gln Ser Glu Lys Ser
1 5 10 15

<210> 26
<211> 15
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: aa of
mut.SF162 cleavage site

<400> 26

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Ser
1 5 10 15

<210> 27

<211> 15

<212> PRT

<213> Human immunodeficiency virus

<220>

<223> Description of Artificial Sequence: aa of native
cleavage site in US4

<400> 27

Ala Pro Thr Gln Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg
1 5 10 15

<210> 28

<211> 5

<212> PRT

<213> Human immunodeficiency virus

<220>

<223> Description of Artificial Sequence: aa of second
cleavage site in US4

<400> 28

Gln Ala Lys Arg Arg
1 5

<210> 29

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: aa of mut.US4
cleavage site

<400> 29

Ala Pro Thr Gln Ala Lys Arg Arg Val Val Gln Arg Glu Lys Ser
1 5 10 15

<210> 30

<211> 1419

<212> DNA

<213> Human immunodeficiency virus

<400> 30

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acacatgcct gtgtaccacac agaccctaac ccacaagaaa tagtattgga aaatgtgaca 180
gaaaattttt acatgtggaa aaataacatg gtagaacaga tgcattgagga tataatcagt 240
ttatggggtc aaagtctaaa gccatgtgta aagttaaccc cactctgtgt tactctacat 300
tgcactaatt tgaagaatgc tactaatacc aagagtagta attggaaaga gatggacaga 360
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gaatatgcac ttttttataa acttgatgta gtaccaatag ataattgataa tacaagctat 480
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tgagagaagt aattatataa atataaagta gtaaaaattg agccattagg agtagcacc 1380
accaaggcaa agagaagagt ggtgcagaga gaaaaaaga 1419

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<210> 31

<211> 1932

<212> DNA

<213> Human immunodeficiency virus

<400> 31

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acacatgcct gtgtaccacac agaccctaac ccacaagaaa tagtattgga aaatgtgaca 180
gaaaattttt acatgtggaa aaataacatg gtagaacaga tgcattgagga tataatcagt 240
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ggagaaataa aaaattgctc tttcaaggct accacaagca taagaaataa gatgcagaaa 420
gaatatgcac ttttttataa acttgatgta gtaccaatag ataattgataa tacaagctat 480
aaattgataa attgtaacac ctcatgcatt acacaggcct gtccaaagggt atcctttgaa 540
ccaattccca tacattattg tgccccggct ggttttgcga ttctaaagtg taatgataag 600
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acaaacttaa	tatacacctt	aattgaagaa	tcgcagaacc	aacaagaaaa	gaatgaacaa	1860
gaattattag	aattggataa	gtgggcaagt	ttgtggaatt	ggtttgacat	atcaaaatgg	1920
ctgtggtata	ta					1932

<210> 32

<211> 2457

<212> DNA

<213> Human immunodeficiency virus

<400> 32

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acacatgcct	gtgtacccac	agaccctaac	ccacaagaaa	tagtatttga	aatgtgaca	180
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ggagaaataa	aaaattgtct	tttcaaggtc	accacaagca	taagaaataa	gatgcagaaa	420
gaatatgcac	ttttttataa	acttgatgta	gtaccaatag	ataatgataa	tacaagctat	480
aaattgataa	attgtaacac	ctcagtcatt	acacaggcct	gtccaaagggt	atcctttgaa	540
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gggagagcat	tttatgcaac	aggagacata	ataggagata	taagacaagc	acattgtaac	900
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gctatagcag	tagctgaggg	gacagatagg	attatagaag	tagcacaaag	aattggtaga	2400
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<210> 33

<211> 1453

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: gp120.modSF162

<400> 33

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cccgtgtgga aggaggccac caccacctg ttctgcgcca gcgacgcca ggccctacgac 180
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gcctgcccc aagtgaactt cgagcccat cccatccact actgcgcccc cgccggcttc 660
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accgtgcagt gcacccacgg catccgcccc gtggtgagca ccagctgct gctgaacggc 780
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<210> 34

<211> 1387

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
gp120.modSF162.delV2

<400> 34

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cccgtgtgga aggaggccac caccacctg ttctgcgcca gcgacgcca ggccctacgac 180
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ggcaaggaga tcagcaaacac caccgagatc ttccgccccg gcggcgggcga catgcgcgac 1320
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<210> 35

<211> 1323

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

gp120.modSF162.delV1V2

<400> 35

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gacatgcgcg acaactggcg cagcgagctg tacaagtaca aggtggtgaa gatcgagccc 1260
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gag

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<210> 36

<211> 2025

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: gp140.modSF162

<400> 36

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gcttgccttca aggtgagctt cgagcccatc cccatccact actgcgcccc cgccggcttc 660
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accgtgcagt gcacccacgg catccgcccc gtggtgagca cccagctgct gctgaacggc 780
agcctggcgg aggagggcgt ggtgatccgc agcgagaact tcaccgacaa cgccaagacc 840
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cgcaagagca tcaccatcgg ccccgggcgc gccttctacg ccaccggcga catcatcggc 960
gacatccgcc aggccactg caacatcagc ggcgagaagt ggaacaacac cctgaagcag 1020
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ggcgggcgacc ccgagatcgt gatgcacagc ttcaactgcg gcggcgagtt cttctactgc 1140
aacagcacc cagctgttcaa cagcacctgg aacaacacca tcggccccaa caacaccaac 1200
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aaggccatgt acgccccccc catccgcggc cagatccgct gcagcagcaa catcaccggc 1320
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ggcgggcgggc acatgcgcga caactggcgc agcgagctgt acaagtacaa ggtggtgaag 1440
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cgcgccgtga ccctgggcgc catgttctctg ggcttctctg gcgccggcgg cagcaccatg 1560
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cagctgctgg gcatctgggg ctgcagcggc aagctgatct gcaccaccgc cgtgccctgg 1800
aacgccagct ggagcaacaa gagcctggac cagatctgga acaacatgac ctggatggag 1860
tgggagcgcg agatcgacaa ctacaccaac ctgatctaca ccctgatcga ggagagccag 1920
aaccagcagg agaagaacga gcaggagctg ctggagctgg acaagtgggc cagcctgtgg 1980
aactggttcg acatcagcaa gtggctgtgg tacatctaac tcgag 2025

```

<210> 37

<211> 1944

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
gp140.modSF162.delV2

<400> 37

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cccgtgtgga aggaggccac caccacctg ttctgcgcca gcgacgccaa ggcctacgac 180
accgaggtgc acaacgtgtg ggccaccac gcctgcgtgc ccaccgaccc caacccccag 240
gagatcgtgc tggagaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 300
cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 360
acccccctgt gcgtgaccct gcaactgga aggaactgga ccgcggcgag atcaagaact gcagcttcaa ggtgggcgcc 480
agcaactgga tcaactgcaa caccagcgtg atcaccagg cctgccccaa ggtgagcttc 540
ggcaagctgc ccatccacta ctgcgcccc cccggtctcg ccatcctgaa gtgcaacgac 600
aagaagttca acggcagcgg cccctgcacc aacgtgagca ccgtgcagtg caccacggc 660
atccgccccg tggtagacac ccagctgctg ctgaacggca gcctggcga ggagggcgtg 720
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agcgtggaga tcaactgcac ccgccccaac aacaacaccc gcaagagcat caccatcggc 840
cccgcccgcg ctttctacgc caccggcgac atcatcggcg acatccgcca ggccccactgc 900
aacatcagcg gcgagaagtg gaacaacacc ctgaagcaga tcgtgaccaa gctgcaggcc 960
cagttcggca acaagaccat cgtgttcaa cagagcagcg gcggcgaccc cgagatcgtg 1020
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agcacctgga acaacaccat cggccccaac gcaccaacg gcaccatcac cctgccctgc 1140
cgcacatcagc agatcatcaa ccgctggcag gaggtgggca aggccatgta cgccccccc 1200
atccgcggcc agatccgctg cagcagcaac atcaccggcc tgctgctgac ccgcgacggc 1260
ggcaaggaga tcagcaacac caccgagatc ttccgccccg gcggcggcga catgcgcgac 1320
aactggcgca gcgagctgta caagtacaag gtggtgaaga tcgagccctt gggcgtggcc 1380
cccaccaagg ccaagcgccg cgtggtgcag cgcgagaagc gcgccgtgac cctgggcgcc 1440

```

```

atgttcctgg gcttcctggg cgccgcccggc agcaccatgg gcgcccgcag cctgaccctg 1500
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gccatcgagg ccagcagca cctgctgcag ctgaccgtgt ggggcatcaa gcagctgcag 1620
gcccgcgtgc tggccgtgga gcgctacctg aaggaccagc agctgctggg catctggggc 1680
tgcagcggca agctgatctg caccaccgcc gtgccctgga acgccagctg gagcaacaag 1740
agcctggacc agatctggaa caacatgacc tggatggagt gggagcgcga gatcgacaac 1800
tacaccaacc tgatctacac cctgatcgag gagagccaga accagcagga gaagaacgag 1860
caggagctgc tggagctgga caagtgggcc agcctgtgga actggttcga catcagcaag 1920
tggctgtggt acatctaact cgag                                     1944

```

<210> 38

<211> 1944

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

gp140.modSF162.delV1/V2

<400> 38

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ccgtgtgga aggaggccac caccacctg ttctgcgcca gcgacgcaa ggcctacgac 180
accgaggtgc acaacgtgtg ggccaccac gcctgcgtgc ccaccgacc caacccccag 240
gagatcgctg tggagaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 300
cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 360
acccccctgt gcgtgaccct gactgcacc aacctgaaga acgccaccaa caccaagagc 420
agcaactgga aggagatgga ccgcggcgag atcaagaact gcagcttcaa ggtgggcgcc 480
ggcaagctga tcaactgcaa caccagcgtg atcaccagg cctgccccaa ggtgagcttc 540
gagcccatcc ccatccacta ctgcgcccc gcgggttcg ccatcctgaa gtgcaacgac 600
aagaagtcca acggcagcgg ccctgcacc aacgtgagca ccgtgcagtg caccacggc 660
atccgccccg tggtagacac ccagctgtg ctgaacggca gcctggccga ggagggcgtg 720
gtgatccgca gcgagaactt caccgacaac aacaacaccc gcaagagcat caccatcggc 780
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ccgggcccgc cttctacgc caccggcgac atcatcggcg acatccgcca ggcccactgc 900
aacatcagcg gcgagaagtg gaacaacacc ctgaagcaga tcgtgaccaa gctgcaggcc 960
cagttcggca acaagaccat cgtgttcaag cagagcagcg gcggcgaccc cgagatcgtg 1020
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agcacctgga acaacaccat cggccccaac aacaccaacg gcaccatcac cctgccctgc 1140
cgcatcaagc agatcatcaa ccgctggcag gaggtgggca aggccatgta cgcccccccc 1200
atccgcggcc agatccgctg cagcagcaac atcaccggcc tgctgctgac ccgcgacggc 1260
ggcaaggaga tcagcaacac caccgagatc ttccgcccc gcggcggcga catgcgcgac 1320
aactggcgca gcgagctgta caagtacaag gtggtgaaga tcgagccctt gggcgtggcc 1380
cccaccaagg ccaagcgccg cgtggtgcag cgcgagaagc gcgccgtgac cctgggcgcc 1440
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gccatcgagg ccagcagca cctgctgcag ctgaccgtgt ggggcatcaa gcagctgcag 1620
gcccgcgtgc tggccgtgga gcgctacctg aaggaccagc agctgctggg catctggggc 1680
tgcagcggca agctgatctg caccaccgcc gtgccctgga acgccagctg gagcaacaag 1740
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tacaccaacc tgatctacac cctgatcgag gagagccaga accagcagga gaagaacgag 1860
caggagctgc tggagctgga caagtgggcc agcctgtgga actggttcga catcagcaag 1920
tggctgtggt acatctaact cgag                                     1944

```

<210> 39

<211> 2025

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
gp140.mut.modSF162

<400> 39

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gcagtcttcg ttctgcccag cgccgtggag aagctgtggg tgaccgtgta ctacggcgtg 120
cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgcca ggcctacgac 180
accgaggtgc acaacgtgtg ggccaccac gcctgcgtgc ccaccgaccc caacccccag 240
gagatcgtgc tggagaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 300
cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 360
acccccctgt gcgtgaccct gactgcacc aacctgaaga acgccaccaa caccaagagc 420
agcaactgga aggagatgga ccgcggcgag atcaagaact gcagcttcaa ggtgaccacc 480
agcatccgca acaagatgca gaaggagtac gccctgttct acaagctgga cgtggtgccc 540
atcgacaacg acaacaccag ctacaagctg atcaactgca acaccagcgt gatcaccag 600
gcctgcccc aagtgagctt cgagcccat cccatccact actgcgcccc cgccggcttc 660
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accgtgcagt gcacccacgg catccgcccc gtggtgagca cccagctgct gctgaacggc 780
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atcgtgacca agctgcagge ccagttcggc aacaagacca tcgtgttcaa gcagagcagc 1080
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aacagcacc agctgttcaa cagcacctgg aacaacacca tcggcccaa caacaccaac 1200
ggcaccatca cctgcccctg ccgcatcaag cagatcatca accgtggca ggaggtgggc 1260
aaggccatgt acgccccccc catccgcggc cagatccgct gcagcagcaa catcacggc 1320
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ggcgggcggg acatgcgcga caactggcgc agcgagctgt acaagtacaa ggtggtgaag 1440
atcgagcccc tgggcgtggc cccaccaag gccaaagcgc gcgtggtgca gcgcgagaag 1500
agcgccgtga ccctgggcgc catgttccctg ggcttccctg gcgccgcgg cagcaccatg 1560
ggcgcccgcga gcctgaccct gaccgtgcag gcccgcagc tgctgagcgg catcgtgcag 1620
cagcagaaca acctgctgcg cgccatcgag gcccgagcag acctgctgca gctgaccgtg 1680
tggggcatca agcagctgca ggcccgcgtg ctggccgtgg agcgctacct gaaggaccag 1740
cagctgctgg gcatctgggg ctgcagcggc aagctgatct gcaccaccgc cgtgccctgg 1800
aacgccagct ggagcaacaa gagcctggac cagatctgga acaacatgac ctggatggag 1860
tgggagcgcg agatcgacaa ctacaccaac ctgatctaca ccctgatcga ggagagccag 1920
aaccagcagg agaagaacga gcaggagctg ctggagctgg acaagtgggc cagcctgtgg 1980
aactggttcg acatcagcaa gtggctgtgg tacatctaac tcgag 2025

```

<210> 40

<211> 1944

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
gp140.mut.modSF162.delV2

<400> 40

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gcagtcttcg ttctgcccag cgccgtggag aagctgtggg tgaccgtgta ctacggcgtg 120
cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgcca ggcctacgac 180
accgaggtgc acaacgtgtg ggccaccac gcctgcgtgc ccaccgaccc caacccccag 240
gagatcgtgc tggagaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 300
cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 360
acccccctgt gcgtgaccct gactgcacc aacctgaaga acgccaccaa caccaagagc 420
agcaactgga aggagatgga ccgcggcgag atcaagaact gcagcttcaa ggtgggcgcc 480
ggcaagctga tcaactgcaa caccagcgtg atcaccaggg cctgccccaa ggtgagcttc 540

```

```

gagcccatcc ccatccacta ctgcgcccc gccggcttcg ccatcctgaa gtgcaacgac 600
aagaagttca acggcagcgg cccctgcacc aacgtgagca ccgtgcagtg caccacggc 660
atccgccccg tggtagcac ccagctgctg ctgaacggca gcctggcga ggagggcgtg 720
gtgatccgca gcgagaactt caccgacaac gccaaagacca tcacgtgca gctgaaggag 780
agcgtggaga tcaactgcac ccgccccaac aacaacaccc gcaagagcat caccatcggc 840
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aacatcagcg gcgagaagtg gaacaacacc ctgaagcaga tcgtgaccaa gctgcaggcc 960
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gcccgcgtgc tggccgtgga gcgctacctg aaggaccagc agctgctggg catctggggc 1680
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agcctggacc agatctggaa caacatgacc tggatggagt gggagcgcg gatcgacaac 1800
tacaccaacc tgatctacac cctgatcgag gagagccaga accagcagga gaagaacgag 1860
caggagctgc tggagctgga caagtgggcc agcctgtgga actggttcga catcagcaag 1920
tggctgtggt acatctaact cgag

```

<210> 41

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

gp140.mut.modSF162.delV1/V2

<400> 41

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gcagtcttcg tttcgcccag cgccgtggag aagctgtggg tgaccgtgta ctacggcgtg 120
cccggtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgcca ggccctacgac 180
accgaggtgc acaacgtgtg ggccaccac gcctgcgtgc ccaccgaccc caacccccag 240
gagatcgtgc tggagaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 300
cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 360
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aaggtgagct tcgagcccat ccccatccac tactgcgccc ccgccggctt cgccatcctg 480
aagtgcacgc acaagaagtt caacggcagc ggcccctgca ccaacgtgag caccgtgcag 540
tgcaccacgc gcatccgccc cgtggtgagc acccagctgc tgctgaacgg cagcctggcc 600
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caggcccact gcaacatcag cggcgagaag tggacaacaa ccctgaagca gatcgtgacc 840
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cccagatcg tgatgcacag cttcaactgc ggcgcgaggt tcttctactg caacagcacc 960
cagctgttca acagcacctg gaacaacacc atcgcccca acaacaccaa cggcaccatc 1020
accctgcccct gccgcatcaa gcagatcatc aaccgtggc aggaggtggg caaggccatg 1080
tacgcccccc ccatccgccc ccagatccgc tgcagcagca acatcaccgg cctgctgctg 1140
acccgcgacg gcggcaagga gatcagcaac accaccgaga tcttcgccc cgccggcgcc 1200
gacatgcgcg acaactggcg cagcgagctg tacaagtaca aggtggtgaa gatcgagccc 1260
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```

```

aacctgctgc ggcgccatcga ggcccagcag cacctgctgc agctgaccgt gtgggggcatc 1500
aagcagctgc aggccccgct gctggccgtg gagcgctacc tgaaggacca gcagctgctg 1560
ggcatctggg gctgcagcgg caagctgatc tgcaccaccg ccgtgccctg gaacgccagc 1620
tggagcaaca agagcctgga ccagatctgg aacaacatga cctggatgga gtgggagcgc 1680
gagatcgaca actacaccaa cctgatctac accctgatcg aggagagcca gaaccagcag 1740
gagaagaacg agcaggagct gctggagctg gacaagtggg ccagcctgtg gaactggttc 1800
gacatcagca agtggctgtg gtacatctaa ctcgag 1836

```

<210> 42

<211> 2025

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
gp140.mut7.modSF162

<400> 42

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cccggtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgcca ggccctacgac 180
accgaggtgc acaacgtgtg ggccacccac gcctgcgtgc ccaccgaccc caacccccag 240
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cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 360
acccccctgt gcgtgaccct gcactgcacc aacctgaaga acgccacca caccaagagc 420
agcaactgga aggagatgga ccgcggcgag atcaagaact gcagcttcaa ggtgaccacc 480
agcatccgca acaagatgca gaaggagtac gccctgttct acaagctgga cgtggtgccc 540
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gcctgcccc aagtgagctt cgagcccatc cccatccact actgcgcccc cgccggcttc 660
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accgtgcagt gcaccacagg catccgcccc gtggtgagca cccagctgct gctgaacggc 780
agcctggccg aggagggcgt ggtgatccgc agcgagaact tcaccgacaa cgccaagacc 840
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cgcaagagca tcaccatcgg ccccgccgc gccttctacg ccaccggcga catcatcggc 960
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aacgccagct ggagcaacaa gagcctggac cagatctgga acaacatgac ctggatggag 1860
tgggagcgcg agatcgacaa ctacaccaac ctgatctaca cctgatcga ggagagccag 1920
aaccagcagg agaagaacga gcaggagctg ctggagctgg acaagtgggc cagcctgtgg 1980
aactggttcg acatcagcaa gtggctgtgg tacatctaac tcgag 2025

```

<210> 43

<211> 1944

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
gp140.mut7.modSF162.delV2

<400> 43

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cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgcaa ggcctacgac 180
accgaggtgc acaacgtgtg ggccaccac gctgctgctg ccaccgacct caacccccag 240
gagatcgctg tggagaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 300
cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 360
acccccctgt gcgtgacctt gcaactgcac aacctgaaga acgccaccaa caccaagagc 420
agcaactgga aggagatgga ccgcggcgag atcaagaact gcagcttcaa ggtggggcgcc 480
ggcaagctga tcaactgcaa caccagcgtg atcaccagg cctgccccaa ggtgagcttc 540
gagcccatcc ccatccacta ctgcgcccc gccggcttcg ccatcctgaa gtgcaacgac 600
aagaagttca acggcagcgg cccctgcacc aacgtgagca ccgtgcagtg caccacggc 660
atccgccccg tggtagcac ccagctgctg ctgaacggca gcctggccga ggagggcgtg 720
gtgatccgca gcgagaactt caccgacaac gccaaagacca tcatcgtgca gctgaaggag 780
agcgtggaga tcaactgcac ccgccccaac aacaacaccc gcaagagcat caccatcggc 840
cccgcccgcg ctttctacgc caccggcgac atcatcggcg acatccgcca ggcccactgc 900
aacatcagcg gcgagaagtg gaacaacacc ctgaagcaga tcgtgaccaa gctgcaggcc 960
cagttcgga acaagaccat cgtgttcaag cagagcagcg gcggcgacct cgagatcgtg 1020
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agcacctgga acaacaccat cggccccaac aacaccaacg gcaccatcac cctgccctgc 1140
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atcccgggcc agatccgctg cagcagcaac atcaccggcc tgctgctgac ccgcgacggc 1260
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cccaccaagg ccatcagcag cgtggtgtag agcgagaaga gcgcccgtgac cctggggcgcc 1440
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tgcagcggca agctgatctg caccaccgac gtgcccctgga acgccagctg gagcaacaag 1740
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tacaccaacc tgatctacac cctgatcgag gagagccaga accagcagga gaagaacgag 1860
caggagctgc tggagctgga caagtgggac agcctgtgga actggttcga catcagcaag 1920
tggctgtggt acatctaact cgag

```

<210> 44

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
gp140.mut7.modSF162.delV1/V2

<400> 44

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cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgcaa ggcctacgac 180
accgaggtgc acaacgtgtg ggccaccac gctgctgctg ccaccgacct caacccccag 240
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cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 360
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aaggtagct tcgagcccat ccccatccac tactgcgccc ccgcccgtt cgccatcctg 480
aagtgaacg acaagaagtt caacggcagc ggcccctgca ccaacgtgag caccgtgcag 540
tgcaccacg gcacccgccc cgtggtgagc acccagctgc tgctgaacgg cagcctggcc 600
gaggagggcg tggtagatcc cagcgagaac ttcaccgaca acgccaagac catcatcgtg 660

```

```

cagctgaagg agagcgtgga gatcaactgc acccgcccca acaacaacac ccgcaagagc 720
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caggcccact gcaacatcag cggcgagaag tggacaaca ccctgaagca gatcgtgacc 840
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cccagatcgg tgatgcacag cttcaactgc ggcggcgagt tcttctactg caacagcacc 960
cagctgttca acagcacctg gaacaacacc atcgcccca acaacaccaa cggcaccatc 1020
accctgccct gccgcatcaa gcagatcatc aaccgctggc aggaggtggg caaggccatg 1080
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acccgcgacg gcggcaagga gatcagcaac accaccgaga tcttccgccc cggcggcggc 1200
gacatgcggc acaactggcg cagcgagctg tacaagtaca aggtggtgaa gatcgagccc 1260
ctgggcgtgg cccccaccaa ggccatcagc agcgtggtgc agagcgagaa gagcgccgtg 1320
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agcctgaccc tgaccgtgca ggcccggcag ctgctgagcg gcacgtgca gcagcagaac 1440
aacctgctgc gcgccatcga ggcccagcag cacctgctgc agctgaccgt gtggggcatc 1500
aagcagctgc aggcccgctg gctggccgtg gagcgctacc tgaaggacca gcagctgctg 1560
ggcatctggg gctgcagcgg caagctgatc tgcaccaccg ccgtgccctg gaacgccagc 1620
tggagcaaca agagcctgga ccagatctgg aacaacatga cctggatgga gtgggagcgc 1680
gagatcgaca actacaccaa cctgatctac accctgatcg aggagagcca gaaccagcag 1740
gagaagaacg agcaggagct gctggagctg gacaagtggg ccagcctgtg gaactgggtc 1800
gacatcagca agtggctgtg gtacatctaa ctcgag 1836

```

<210> 45

<211> 2025

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 gp140.mut8.modSF162

<400> 45

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gcagtcttcg ttctgcccag cgccgtggag aagctgtggg tgaccgtgta ctacggcggtg 120
cccggtgtga aggaggccac caccaccctg ttctgcgcca gcgacgcca ggccctacgac 180
accgaggtgc acaacgtgtg ggccaccac gcctgcgtgc ccaccgacce caacccccag 240
gagatcgtgc tggagaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 300
cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 360
acccccctgt gcgtgaccct gcaactgcacc aacctgaaga acgccaccaa caccaagagc 420
agcaactgga aggagatgga ccgcggcgag atcaagaact gcagcttcaa ggtgaccacc 480
agcatccgca acaagatgca gaaggagtac gccctgttct acaagctgga cgtggtgccc 540
atcgacaacg acaacaccag ctacaagctg atcaactgca acaccagcgt gatcacccag 600
gcctgcccc aagtgcgctt cgagcccact cccatccact actgcgcccc cgccggcttc 660
gccatcctga agtgcaacga caagaagttc aacggcagcg gccctgcac caacgtgagc 720
accgtgcagt gcaccacagg catccgcccc gtggtgagca ccagctgct gctgaacggc 780
agcctggccg aggagggcgt ggtgatccgc agcgagaact tcaccgacaa cgccaagacc 840
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ggcggcgacc ccgagatcgt gatgcacagc ttcaactgcg gcggcgagtt cttctactgc 1140
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ggcaccatc ccctgccctg ccgcatcaag cagatcatca accgctggca ggaggtgggc 1260
aaggccatgt acgccccccc catccggcgc cagatccgct gcagcagcaa catcaccggc 1320
ctgctgctga cccgcgacgg cggcaaggag atcagcaaca ccaccgagat cttccgcccc 1380
ggcggcgggc acatgcgcga caactggcgc agcgagctgt acaagtacaa ggtggtgaag 1440
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agcggcgtga ccctggggcg catgttctct ggttctctgg gcgcccggc cagcaccatg 1560
ggcggccgca gcctgaccct gaccgtgcag gcccgccagc tgctgagcgg catcgtgcag 1620
cagcagaaca acctgctgcg cgccatcag gccagcagc acctgctgca gctgaccgtg 1680

```

```

tggggcatca agcagctgca ggcccgcgtg ctggccgtgg agcgctacct gaaggaccag 1740
cagctgctgg gcatctgggg ctgcagcggc aagctgatct gcaccaccgc cgtgccctgg 1800
aacgccagct ggagcaacaa gagcctggac cagatctgga acaacatgac ctggatggag 1860
tgggagcgcg agatcgacaa ctacaccaac ctgatctaca ccctgatcga ggagagccag 1920
aaccagcagg agaagaacga gcaggagctg ctggagctgg acaagtgggc cagcctgtgg 1980
aactggttcg acatcagcaa gtggctgtgg tacatctaac tcgag 2025

```

<210> 46

<211> 1944

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

gp140.mut8.modSF162.delV2

<400> 46

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gcagtcttcg ttctgcccag cgccgtggag aagctgtggg tgaccgtgta ctacggcgtg 120
cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgcaa ggcctacgac 180
accgaggtgc acaacgtgtg ggccacccac gcctgcgtgc ccaccgaccc caacccccag 240
gagatcgctg tggagaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 300
cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 360
acccccctgt gcgtgaccct gcaactgcacc aacctgaaga acgccaccaa caccaagagc 420
agcaactgga aggagatgga ccgcggcgag atcaagaact gcagcttcaa ggtgggcgcc 480
ggcaagctga tcaactgcaa caccagcgtg atcaccagg cctgccccaa ggtgagcttc 540
gagcccatcc ccatccacta ctgcgccccg gccggcttcg ccatacctgaa gtgcaacgac 600
aagaagttca acggcagcgg cccctgcacc aacgtgagca ccgtgcagtg caccacggc 660
atccgccccg tggtagacac ccagctgctg ctgaacggca gcctggccga ggagggcgtg 720
gtgatccgca gcgagaactt caccgacaac gccaagacca tcacgtgca gctgaaggag 780
agcgtggaga tcaactgcac ccgccccaac aacaacaccc gcaagagcat caccatcggc 840
cccgcccgcg ccttctacgc caccggcgac acatccggcg acatccgcca ggcccactgc 900
aacatcagcg gcgagaagtg gaacaacacc ctgaagcaga tcgtgaccaa gctgcaggcc 960
cagttcggca acaagaccat cgtgttcaag cagagcagcg gcggcgaccc cgagatcgtg 1020
atgcacagct tcaactgcgg cggcgagttc ttctactgca acagcaccca gctgttcaac 1080
agcacctgga acaacaccat cggccccaac aacaccaacg gcaccatcac cctgccctgc 1140
cgcataaagc agatcatcaa ccgctggcag gagtgaggca aggccatgta cggccccccc 1200
atccgcggcc agatccgctg cagcagcaac atcaccggcc tgctgctgac ccgcgacggc 1260
ggcaaggaga tcagcaacac caccgagatc ttccgccccg gcggcgccga catgcgcgac 1320
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cccaccatcg ccatcagcag cgtggtgagc agcgagaaga gcgccgtgac cctgggcgcc 1440
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tacaccaacc tgatctacac cctgatcgag gagagccaga accagcagga gaagaacgag 1860
caggagctgc tggagctgga caagtgggccc agcctgtgga actggttcga catcagcaag 1920
tggctgtggg acatctaact cgag 1944

```

<210> 47

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

gp140.mut8.modSF162.delV1/V2

<400> 47

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cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgcca ggcctacgac 180
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cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 360
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aaggtgagct tcgagcccat ccccatccac taactgcgcc ccgccggctt cgccatcctg 480
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caggccact gcaacatcag cggcgagaag tggaacaaca ccctgaagca gatcgtgacc 840
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gacatgcgcg acaactggcg cagcgagctg tacaagtaca aggtggtgaa gatcgagccc 1260
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gagatcgaca actacaccaa cctgatctac accctgatcg aggagagcca gaaccagcag 1740
gagaagaacg agcaggagct gctggagctg gacaagtggg ccagcctgtg gaactggttc 1800
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1836

<210> 48

<211> 2547

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: gp160.modSF162

<400> 48

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cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgcca ggcctacgac 180
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cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 360
acccccctgt gcgtgaccct gcaactgcac aacctgaaga acgccacca caccaagagc 420
agcaactgga aggagatgga ccgcggcgag atcaagaact gcagcttcaa ggtgaccacc 480
agcatccgca acaagatgca gaaggagtac gccctgttct acaagctgga cgtggtgccc 540
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gcctgcccc aagtgagctt cgagcccatc cccatccact actgcgccc cgccggcttc 660
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accgtgcagt gcaccacgg catccgcccc gtggtgagca ccagctgct gctgaacggc 780
agcctggccg aggagggcgt ggtgatccgc agcgagaact tcaccgaca cgccaagacc 840
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cgcaagagca tcaccatcgg ccccgccgc gccttctacg ccaccggcga catcatcggc 960
gacatccgcc agggccactg caacatcagc ggcgagaagt ggaacaacac cctgaagcag 1020

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aacagcaccc agctgttcaa cagcacctgg aacaacacca tcggcccaa caacaccaac 1200
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aaggccatgt acgccccccc catccgcggc cagatccgct gcagcagcaa catcacgggc 1320
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tgggagcgcg agatcgacaa ctacaccaac ctgatctaca ccctgatcga ggagagccag 1920
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gccgtgagcc tgttcgacgc catcgccatc gccgtggcgg agggcaccga ccgcatcatc 2460
gaggtggccc agcgcacggy ccgcgccttc ctgcacatcc cccgccgcat ccgccagggc 2520
ttcgagcgcg ccctgctgta actcgag

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<210> 49

<211> 2466

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

gp160.modSF162.delV2

<400> 49

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cccggtgtgga aggaggccac caccacctg ttctgcgcca gcgacgcaa ggcctacgac 180
accgaggtgc acaacgtgtg ggccaccac gcctgcgtgc ccaccgaccc caacccccag 240
gagatcgtgc tggagaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 300
cagatgcacg aggacatcat cagcctgtgg caccagagcc tgaagccctg cgtgaagctg 360
acccccctgt gcgtgaccct gcaactgcac aacctgaaga acgccaccaa caccaagagc 420
agcaactgga aggagatgga ccgcggcgag atcaagaact gcagcttcaa ggtgggcgcc 480
ggcaagctga tcaactgcaa caccagcgtg atcaccagc cctgccccaa ggtgagcttc 540
gagcccatcc ccattcacta ctgcgcccc gccggtctcg ccattcctgaa gtgcaacgac 600
aagaagttca acggcagcgg ccctgcacc aacgtgagca ccgtgcagtg caccacggc 660
atccgccccg tgggtgagcac ccagctgctg ctgaacggca gcctggccga ggagggcgtg 720
gtgatccgca gcgagaactt caccgacaac gccaaagacca tcatcgtgca gctgaaggag 780
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accgtgcagg cccgccagct gctgagcggc atcgtgcagc agcagaacaa cctgctgcgc 1560
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ctcgag

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<210> 50

<211> 2358

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

gp160.modSF162.delV1/V2

<400> 50

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cccggtgtgga aggaggccac caccacctg ttctgcgcca gcgacgcca ggcctacgac 180
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aagggtgagct tcgagcccat ccccatccac tactgcgccc ccgcccggctt cgccatcctg 480
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tggagcaaca agagcctgga ccagatctgg aacaacatga cctggatgga gtgggagcgc 1680

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gacatcagca agtggctgtg gtacatcaag atcttcatca tgatcgtggg cggcctgggtg 1860
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gccctgctgt aactcgag
2358

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<210> 51

<211> 1494

<212> DNA

<213> Human immunodeficiency virus

<400> 51

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acacatgcct gtgtaccac agaccccaac ccacaggaag taaatttaac aaatgtgaca 180
gaaaatttta acatgtggaa aaataacatg gtggaacaga tgcagttaga tataatcagt 240
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gaatattctc tcttctataa acttgatgta gtaccaatag ataagataa tgctagctat 540
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aagttcaatg gaacaggacc atgtaaaaat gtcagcacag tacaatgcac acatggaatt 720
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tttgggaata ataaaacaat aatctttaat tcctcctcag gaggggaccc agaaattgta 1080
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ccatgcagaa taagacaaat tataaacatg tggcaagaag taggaaaagc aatgtatgcc 1260
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aacatgaagg acaattggag aagtgaatta tataaatata aagtagtaag aattgaacca 1440
ttaggagtag caccaccca ggcaaagaga agagtgggtg aaagagagaa aaga 1494

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<210> 52

<211> 2007

<212> DNA

<213> Human immunodeficiency virus

<400> 52

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acacatgcct gtgtaccac agaccccaac ccacaggaag taaatttaac aaatgtgaca 180
gaaaatttta acatgtggaa aaataacatg gtggaacaga tgcagttaga tataatcagt 240
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tgtactgata agttgacagg tagtactaat ggcacaaata gtactagtgg cactaatagt 360
actagtggca ctaatagtac tagtactaat agtactgata gttgggaaaa gatgccagaa 420
ggagaaataa aaaactgctc tttcaatatc accacaagtg taagagataa agtgcagaaa 480

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gaatattctc tcttctataa acttgatgta gtaccaatag ataatgataa tgctagctat 540
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ccaattccca tacattattg tgccccggct gggtttgcga ttctaaagtg taaagataag 660
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cttagatctg aaaatttcac agacaatgct aaaaccataa tagtacagct gaatgaatct 840
gtagaaatta attgtataag acccaacaat aatacaagaa aaagtataca tataggacca 900
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gaaattggca attatacagg cttaatatat aatttaattg aaatagcaca aaaccagcaa 1920
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<210> 53

<211> 2532

<212> DNA

<213> Human immunodeficiency virus

<400> 53

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tgtactgata agttgacagg tagtactaat ggcacaaata gtactagtgg cactaatagt 360
actagtggca ctaatagtag tagtactaat agtactgata gttgggaaaa gatgccagaa 420
ggagaaataa aaaactgctc tttcaatatc accacaagtg taagagataa agtgcagaaa 480
gaatattctc tcttctataa acttgatgta gtaccaatag ataatgataa tgctagctat 540
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<210> 54

<211> 1599

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: gp120.modUS4

<400> 54

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tacaaggtgg  tgccgcatcg  gccctgggc  gtggccccc  cccaggccaa  gcgcccgcgtg  1560
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<210> 55

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

gp120.modUS4.del 128-194

<400> 55

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aaggtgagct tcgagcccat ccccatccac tactgcgccc ccgcccggctt cgccatcctg 480
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<210> 56

<211> 2112

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: gp140.modUS4

<400> 56

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2112

<210> 57

<211> 2112

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

gp140.mut.modUS4

<400> 57

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gccgaggccc acaacgtgtg ggccaccac gcctgcgtgc ccaccgaccc caacccccag 240
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 ggatcctcta ga 2112

<210> 58
 <211> 2181
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: gp140TM.modUS4

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<210> 59
 <211> 1818
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 gp140.modUS4.delV1/V2

<400> 59

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1818

<210> 60

<211> 2031

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

gp140.modUS4.delV2

<400> 60

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cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgcca ggcttacaag 180
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<210> 61

<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

gp140.mut.modUS4.delV1/V2

<400> 61

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1818

<210> 62

<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

gp140.modUS4.del 128-194

<400> 62

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gagcgctacc tgaaggacca gcagctgctg ggcattctgg gctgcagcgg caagctgatc 1560
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gacaagtggg ccagcctgtg gaactggttc gacatcacca actggctgtg gtacatctaa 1800
gatatcggat cctctaga
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1818

<210> 63

<211> 1863

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

gp140.mut.modUS4.del 128-194

<400> 63

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gcagtcttcg tttcgcccag cgccaccacc gtgctgtggg tgaccgtgta ctacggcggtg 120
cccggtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgcca ggcttacaag 180
gccgaggccc acaacgtgtg ggccacccac gcctgcgtgc ccaccgaccc caacccccag 240
gaggtgaacc tgaccaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 300
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```

cagatgcatg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 360
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aaggtgagct tcgagcccat ccccatccac tactgcgccc ccgccggtt cgccatcctg 480
aagtgaagg acaagaagtt caacggcacc ggcccctgca agaacgtgag caccgtgcag 540
tgcaccacg gcattcgccc cgtggtgagc acccagctgc tgcgaacgg cagcctggcc 600
gaggaggaga tcgtgctgcg ctccgagaac ttcaccgaca acgccaagac catcatcgtg 660
cagctgaacg agtccgtgga gatcaactgc atccgcccc acaacaacac gcgtaagagc 720
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caggcccact gcaacatcag caaggccaac tggaccaaca cctcagagca gatcgtggag 840
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gcccagaacc agcaggagaa gaacgagcag gagctgctgg agctggacaa gtggggccagc 1800
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aga

```

<210> 64

<211> 2634

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: gp160.modUS4

<400> 64

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cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgcaa ggcttacaag 180
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aacagcacca gcggcaccaa cagcaccagc ggcaccaaca gcaccagcac caacagcacc 480
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aaggagaacg acaccatcat cctgccttgc cgcattccgc agatcatcaa catgtggcag 1320

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gagggtgggca aggccatgta cgcccccccc atccgcggcc agatcaagtg cagcagcaat 1380
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accgaccgca tcatcgagat cgtgcagcgc atcttcgcg ccgtgatcca catccccgc 2580
cgcacccgcc agggcctgga gcgcgcctg ctgtaagata tcggatctc taga 2634

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<210> 65

<211> 2538

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

gp160.modUS4.delV1

<400> 65

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cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgcaa ggcttacaag 180
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tgcaacacca gcgtgatcac ccaggcctgc ccaagggtga gcttcgagcc catccccatc 600
cactactgcg cccccgcgg cttegccatc ctgaagtgca aggacaagaa gttcaacggc 660
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accgtgcagg cccgccagct gctgagcggc atcgtgcagc agcagaacaa cctgctgcgc 1620
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cgcgcctgta tccacatccc ccgcgcgcat cgccagggcc tggagcgcgc cctgctgtaa 2520
gatatcgcat cctctaga
2538

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<210> 66

<211> 2553

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
gp160.modUS4.delV2

<400> 66

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cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgcaa ggcttacaag 180
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aacagcacca gcggcaccaa cagcaccagc ggcaccaaca gcaccagcac caacagcacc 480
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<210> 67

<211> 2340

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

gp160.modUS4.delV1/V2

<400> 67

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cccggtgtgga	aggaggccac	caccaccctg	ttctgcgcca	gcgacgccaa	ggcttacaag	180
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 cccgcgcgca tccgccaggg cctggagcgc gccctgctgt aagatatcgg atcctctaga 2340

<210> 68

<211> 2385

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 gp160.modUS4del 128-194

<400> 68

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 aaggtgagct tcgagcccat ccccatccac tactgcgccc ccgcccggctt cgccatcctg 480
 aagtgaagg acaagaagtt caacggcacc ggcccctgca agaacgtgag caccgtgcag 540
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 cagctgaacg agtccgtgga gatcaactgc atccgcccga acaacaacac gcgtaagagc 720
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 caggcccaact gcaacatcag caaggccaac tggaccaaca ccctcgagca gatcgtggag 840
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<210> 69

<211> 144

<212> DNA

<213> Human immunodeficiency virus

<400> 69

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 aaggccatgt acgccccccc catccgcggc cagatcaagt gcagcagcaa catcaccggc 120
 ctgctgctga cccgcgacgg cggc 144

<210> 70

<211> 144

<212> DNA

<213> Human immunodeficiency virus

<400> 70

ggaactatca cactcccatg cagaataaaa caaattataa acaggtggca ggaagtagga 60
 aaagcaatgt atgcccctcc catcagagga caaattagat gtcacatcaa tattacagga 120
 ctgctattaa caagagatgg tggt 144

<210> 71

<211> 144

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic Env
 US4 common region

<400> 71

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 aaggccatgt acgccccccc catccgcggc cagatcaagt gcagcagcaa catcaccggc 120
 ctgctgctga cccgcgacgg cggc 144

<210> 72

<211> 144

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic Env
 SF162 common region

<400> 72

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 aaggccatgt acgccccccc catccgcggc cagatccgct gcagcagcaa catcaccggc 120
 ctgctgctga cccgcgacgg cggc 144

<210> 73

<211> 4766

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 gp160.modUS4.gag.modSF2

<400> 73

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 cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgcaa ggcttacaag 180
 gccgagggccc acaacgtgtg ggccaccac gcctgcgtgc ccaccgaccc caacccccag 240
 gaggtgaacc tgaccaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 300
 cagatgcatg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 360

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gacagctggg	agaagatgcc	cgaggcgag	atcaagaact	gcagcttcaa	catcaccacc	540
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agaattcaga ctcgagcaag tctaga
4766

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<210> 74

<211> 4689

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
gp160.modSF162.gag.modSF2

<400> 74

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<210> 75

<211> 4472

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

gp160.modUS4.delV1/V2.gag.modSF2

<400> 75

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cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgcaa ggcttacaag 180
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gaggtgaacc tgaccaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 300
cagatgcatg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgggcgcc 360
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```

```

caccagcacc ctgcaggagc agatcggctg gatgaccaac aaccccccca tccccgtggg 3720
cgagatctac aagcgggtgga tcatcctggg cctgaacaag atcgtgcgga tgtacagccc 3780
caccagcatc ctggacatcc gccaggggccc caaggagccc ttccgcgact acgtggaccg 3840
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ccagtaagaa ttcagactcg agcaagtcta ga
4472

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<210> 76

<211> 4608

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

gp160.modSF162.delV2.gag.modSF2

<400> 76

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agcaactgga aggagatgga ccgcggcgag atcaagaact gcagcttcaa ggtgggcgcc 480
ggcaagctga tcaactgcaa caccagcgtg atcaccagg cctgccccaa ggtgagcttc 540
gagcccatcc ccatccacta ctgcgcccc gcgggcttcg ccctcctgaa gtgcaacgac 600
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<210> 77

<211> 1680

<212> DNA

<213> Human immunodeficiency virus

<400> 77

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atggaaaagg aagggaatat ttcaaaaatt gggcctgaaa atccatacaa tactccagta 180
tttgctataa agaaaaaaga cagtactaaa tggagaaaac tagtagattt cagagaactt 240
aataaaagaa ctcaagactt ctgggaagtt cagttaggaa taccacacc cgcagggtta 300
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gataaagact ttagaaagta tactgcattt accataccta gtataaaca tgagacacca 420
gggattagat atcagtacaa tgtgctgcc cagggatgga aaggatcacc agcaatatcc 480
caaagtagca tgacaaaaat cttagagcct tttagaaaac agaattccga catagttatc 540

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catcagaaag aacctccatt cctttggatg gggttatgaac tccatcctga taaatggaca 720
gtacagccta taatgctgcc agaaaaagac agctggactg tcaatgacat acagaagtta 780
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ataatagagc agttaataaa aaaggaaaag gtctacctgg catgggtacc agcacacaaa 1620
ggaattggag gaaatgaaca agtagataaa ttagtcagtg ctggaatcag gaaagtacta 1680

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<210> 78

<211> 1865

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GP1

<400> 78

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gccagccgcg agctggagcg ctctcgccgtg aaccccgccc tgctggagac cagcgagggc 180
tgccgccaga tcctgggcca gctgcagccc agcctgcaga ccggcagcga ggagctgcgc 240
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gtgcagaacc tgcagggcca gatggtgcac caggccatca gccccgcac cctgaacgcc 480
tgggtgaagg tgggtggagga gaaggccttc agccccgagg tgatcccat gttcagcgcc 540
ctgagcgagg gcgccacccc ccaggacctg aacacgatgt tgaacaccgt gggcgccac 600
caggccgcca tgcagatgct gaaggagacc atcaacgagg aggcgcgcca gtgggaccgc 660
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gcaacctgct gaccagatc ggctgcaccc tgaacttccc catcagcccc atcgagacgg 1800

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tgcccggtgaa gctgaagccg gggatggacg gcccgaaggt caagcagtggt cccctgtaag 1860
aattc 1865

<210> 79

<211> 1865

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GP2

<400> 79

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gccagccgcg agctggagcg cttcgccgtg aaccccggcc tgctggagac cagcgagggc 180
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gactacgtgg accgcttcta caagaccctg cgcgctgagc aggcagcca ggacgtgaag 960
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ggccccggcc acaaggcccc cgtgctggcc gaggcgatga gccaggtgac gaacccggcg 1140
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ccaacagccc caccagaaga gagcttcagg tttggggagg agaaaacaac tccctctcag 1440
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aacgacccct cgtcacagta aggatcgggg ggcaactcaa ggaagcgctg ctcgatacag 1560
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gtggacataa agctataggt acagtattag taggacctac acctgtcaac ataattggaa 1740
gaaatctgtt gaccagatc ggctgcacct tgaacttccc catcagccct attgagacgg 1800
tgcccggtgaa gttgaagccg gggatggacg gcccgaaggt caagcaatgg ccattgtaag 1860
aattc 1865

<210> 80

<211> 2305

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
FS(+) .proinact.RTopt.YM

<400> 80

gcgcccgcca aggacaccaa atgaaagatt gcactgagag acaggctaatt tttttaggga 60
agatctggcc ttcctacaag ggaaggccag ggaattttct tcagagcaga ccagagccaa 120
cagccccacc agaagagagc ttcaggtttg gggaggagaa aacaactccc tctcagaagc 180
aggagccgat agacaaggaa ctgtatcctt taacttcctt cagatcactc tttggcaacg 240

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accctcgtc acaataagga tcgggggggca actcaaggaa gcgctgctcg atacaggagc 300
agatgataca gtattagaag aaatgaattt gccaggaaaa tggaaaccaa aaatgatagg 360
ggggatcggg ggcttcatca aggtgaggca gtacgaccag atacctgtag aaatctgtgg 420
acataaagct ataggtacag tattagtagg acctacacct gtcaacataa ttggaagaaa 480
tctgttgacc cagatcggct gcaccttgaa cttccccatc agccctattg agacggtgcc 540
cgtgaagttg aagccgggga tggacggccc caaggtcaag caatggccat tgaccgagga 600
gaagatcaag gccctggtgg agatctgcac cgagatggag aaggagggca agatcagcaa 660
gatcggcccc gagaacccct acaacacccc cgtgttcgcc atcaagaaga aggacagcac 720
caagtggcgc aagctggtgg acttccgcga gctgaacaag cgcacccagg acttctggga 780
ggtgcagctg ggcattcccc accccgcccg cctgaagaag aagaagagcg tgaccgtgct 840
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caccaccaac cagaagaccg agctgcaggc catccacctg gccctgcagg acagcggcct 1980
ggaggtgaac atcgtgaccg acagccagta cgccctgggc atcatccagg cccagcccga 2040
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gtacctggcc tgggtgcccg cccacaaggg catcggcggc aacgagcagg tggacaagct 2160
ggtgagcgcc ggcattccga aggtgctgtt cctgaacggc atcgatggcg gcatcgtgat 2220
ctaccagtac atggacgacc tgtacgtggg cagcggcggc cctaggatcg attaaaagct 2280
tcccggggct agcaccgggtg aattc

```

<210> 81

<211> 2299

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

FS(+).proinact.RTopt.YMWM

<400> 81

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gcggccgcga aggacaccaa atgaaagatt gcaactgagag acaggctaatt tttttagggg 60
agatctggcc ttcctacaag ggaaggccag ggaattttct tcagagcaga ccagagccaa 120
cagccccacc agaagagagc ttcaggtttg gggaggagaa aacaactccc tctcagaagc 180
aggagccgat agacaaggaa ctgtatcctt taacttccct cagatcactc tttggcaacg 240
accctcgtc acaataagga tcgggggggca actcaaggaa gcgctgctcg atacaggagc 300
agatgataca gtattagaag aaatgaattt gccaggaaaa tggaaaccaa aaatgatagg 360
ggggatcggg ggcttcatca aggtgaggca gtacgaccag atacctgtag aaatctgtgg 420
acataaagct ataggtacag tattagtagg acctacacct gtcaacataa ttggaagaaa 480
tctgttgacc cagatcggct gcaccttgaa cttccccatc agccctattg agacggtgcc 540
cgtgaagttg aagccgggga tggacggccc caaggtcaag caatggccat tgaccgagga 600
gaagatcaag gccctggtgg agatctgcac cgagatggag aaggagggca agatcagcaa 660
gatcggcccc gagaacccct acaacacccc cgtgttcgcc atcaagaaga aggacagcac 720
caagtggcgc aagctggtgg acttccgcga gctgaacaag cgcacccagg acttctggga 780

```

```

ggtgcagctg ggcattcccc accccgcccg cctgaagaag aagaagagcg tgaccgtgct 840
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gctgcacccc gacaagtggg ccgtgcagcc catcatgctg cccgagaagg acagctggac 1260
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caaggccggc tacgtgaccg accggggccg gcagaagggt gtgagcatcg ccgacaccac 1920
caaccagaag accgagctgc aggccatcca cctggccctg caggacagcg gcctggaggt 1980
gaacatcgtg accgacagcc agtacgccct gggcatcatc caggcccagc ccgacaagag 2040
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cgccggcatc cgcaacgtgc tgttcctgaa cggcatcgat ggcggcacatc tgatctacca 2220
gtacatggac gacctgtacg tgggcagcgg cggccctagg atcgattaaa agcttcccgg 2280
ggctagcacc ggtgaattc

```

<210> 82

<211> 2306

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

FS (-).protmod.RTopt.YM

<400> 82

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aggacctggc cttcctgcag ggcaaggccc gcgagttcag cagcgagcag acccgcgcca 120
acagcccac ccgcccgcag ctgcagggtgt gggcgggcga gaacaacagc ctgagcgagg 180
ccggcgccga ccgcccaggc accgtgagct tcaacttccc ccagatcacc ctgtggcagc 240
gccccctggt gacctcagg atcggcggcc agtcaagga ggcgctgctc gacaccggcg 300
ccgacgacac cgtgctggag gagatgaacc tgcccggcaa gtggaagccc aagatgatcg 360
gcgggatcgg gggcttcac aaggtgcggc agtacgacca gatccccgtg gagatctgcg 420
gccacaaggc catcggcacc gtgctggtgg gccccacccc cgtgaacatc atcgcccgca 480
acctgctgac ccagatcggc tgcaccctga acttccccat cagccccatc gagacgggtg 540
ccgtgaagct gaagccgggg atggacggcc ccaaggtcaa gcagtggccc ctgaccgagg 600
agaagatcaa ggccctgggt gagatctgca ccgagatgga gaaggagggc aagatcagca 660
agatcgcccc cgagaacccc tacaacaccc ccgtgttcgc catcaagaag aaggacagca 720
ccaagtggcg caagctggtg gacttccgcg agtgaacaa gcgcacccag gacttctggg 780
agggtcagct gggcatcccc caccgcggcg gcctgaagaa gaagaagagc gtgaccgtgc 840
tggacgtggg cgacgcctac ttcagcgtgc ccctggacaa ggacttccgc aagtacaccg 900
ccttcaccat ccccgacatc aacaacgaga cccccggcat ccgctaccag tacaacgtgc 960
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gctacgagct gcaccccgac aagtggaccg tgcagcccat catgctgccc gagaaggaca 1260
gctggaccgt gaacgacatc cagaagctgg tgggcaagct gaactgggccc agccagatct 1320

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acgccggcat caaggtgaag cagctgtgca agctgctgcg cggcaccaag gccctgaccg 1380
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ccggcaagta cggccgcatg cgcggcgccc acaccaacga cgtgaagcag ctgaccgagg 1620
ccgtgcagaa ggtgagcacc gagagcatcg tgatctgggg caagatcccc aagttcaagc 1680
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tgggtgagcg cggcatccgc aaggtgctgt tcctgaacgg catcgatggc ggcacgtgta 2220
tctaccagta catggacgac ctgtacgtgg gcagcggcgg ccctaggatc gattaaaagc 2280
ttcccggggc tagcaccggt gaattc

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2306

<210> 83
 <211> 2300
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 FS(-).protmod.RTopt.YMWM

```

<400> 83
gcgccgcgca aggacaccaa atgaaagatt gcaactgagag acaggctaatt ttcttccgcg 60
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acagcccac ccgccgcgag ctgcaggtgt ggggcggcga gaacaacagc ctgagcgagg 180
cggcgccga ccgccagggc accgtgagct tcaacttccc ccagatcacc ctgtggcagc 240
gccccctggt gaccatcagg atcggcggcc agctcaagga ggcgtgctc gacaccggcg 300
ccgacgacac cgtgctggag gagatgaacc tgcccgcaa gtggaagccc aagatgatcg 360
gcgggatcgg gggcttcatc aaggtgcggc agtacgacca gatccccgtg gagatctgcg 420
gccacaaggc catcggcacc gtgctggtgg gccccacccc cgtgaacatc atcggccgca 480
acctgctgac ccagatcggc tgcacctga acttccccat cagccccatc gagacggtgc 540
ccgtgaagct gaagccgggg atggacggcc ccaaggtcaa gcagtggccc ctgaccgagg 600
agaagatcaa ggccctgggt gagatctgca ccgagatgga gaaggagggc aagatcagca 660
agatcgggcc cgagaacccc tacaacaccc ccgtgttcgc catcaagaag aaggacagca 720
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agctgcaccc cgacaagtgg accgtgcagc ccatcatgct gcccgagaag gacagctgga 1260
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gccagggcca gtggacctac cagatctacc aggagccctt caagaacctg aagaccggca 1560
agtacgccc catgcgcggc gcccacacca acgacgtgaa gcagctgacc gaggccgtgc 1620
agaaggtgag caccgagagc atcgtgatct ggggcaagat cccaagtgc aagctgcccc 1680
tccagaagga gacctgggag gcctgggtgga tggagtactg gcaggccacc tggatccccg 1740
agtgggagtt cgtgaacacc cccccctgg tgaagctgtg gtaccagctg gagaaggagc 1800
ccatcgtggg cgccgagacc ttctacgtgg acggcgccgc caaccgcgag accaagctgg 1860

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gcaaggccgg ctacgtgacc gaccggggcc ggcagaaggt ggtgagcatc gccgacacca 1920
ccaaccagaa gaccgagctg caggccatcc acctggccct gcaggacagc ggccctggagg 1980
tgaacatcgt gaccgacagc cagtacgccc tgggcatcat ccaggccagc cccgacaaga 2040
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tggcctgggt gcccggccac aagggtcatcg gcggcaacga gcaggtggac aagctgggtga 2160
gcgcccggcat ccgcaagggt ctgttcctga acggcatcga tggcggcatc gtgatctacc 2220
agtacatgga cgacctgtac gtgggcagcg gcggccctag gatcgattaa aagcttcccg 2280
gggctagcac cggatgaattc
2300

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<210> 84

<211> 2312

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
FS (-) .protmod.RTopt (+)

<400> 84

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aggacctggc cttcctgcag ggcaaggccc gcgagttcag cagcgagcag acccgcgcca 120
acagcccac ccgcccgcgag ctgcagggtgt ggggcggcga gaacaacagc ctgagcgagg 180
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gccccctggt gaccatcagg atcggcggcc agctcaagga ggcgctgctc gacaccggcg 300
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gcgggatcgg gggcttcac aagggtgcggc agtacgacca gatccccgtg gagatctgcg 420
gccacaaggc catcggcacc gtgctgggtgg gcccaccccc cgtgaacatc atcgcccgca 480
acctgctgac ccagatcggc tgcacctga acttccccat cagccccatc gagacgggtgc 540
ccgtgaagct gaagccgggg atggacggcc ccaagggtcaa gcagtggccc ctgaccgagg 600
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ccaagtggcg caagctgggt gacttccgcg agctgaacaa gcgcacccag gacttctggg 780
agggtcagct gggcatcccc caccgcgcg gcctgaagaa gaagaagagc gtgaccgtgc 840
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tgggcagcga cctggagatc ggccagcacc gcaccaagat cgaggagctg cgccagcacc 1140
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tcgtgatcta ccagtacatg gacgacctgt acgtgggcag ccggcgccct aggatcgatt 2280
aaaagcttcc cggggctagc accggtgaat tc
2312

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<210> 85
 <211> 306
 <212> DNA
 <213> Human immunodeficiency virus

<400> 85
 atggagccag tagatcctag attagagccc tggaagcatc caggaagtca gcctaagact 60
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 aaaggcttag gcatctccta tggcaggaag aagcggagac agcgacgaag agctcctcca 180
 gacagtgagg ttcatcaagt ttctctacca aagcaacccg cttcccagcc ccaagggggac 240
 ccgacaggcc cgaaggaatc gaagaagaag gtggagagag agacagagac agatccagtc 300
 cattag 306

<210> 86
 <211> 101
 <212> PRT
 <213> Human immunodeficiency virus

<400> 86
 Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
 1 5 10 15
 Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
 20 25 30
 His Cys Gln Val Cys Phe Ile Thr Lys Gly Leu Gly Ile Ser Tyr Gly
 35 40 45
 Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala Pro Pro Asp Ser Glu Val
 50 55 60
 His Gln Val Ser Leu Pro Lys Gln Pro Ala Ser Gln Pro Gln Gly Asp
 65 70 75 80
 Pro Thr Gly Pro Lys Glu Ser Lys Lys Lys Val Glu Arg Glu Thr Glu
 85 90 95
 Thr Asp Pro Val His
 100

<210> 87
 <211> 306
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: tat.SF162.opt

<400> 87
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 aagggccttg gcatcagcta cggccgcaag aagcggccgc agcgccgccg cgcccccccc 180
 gacagcgagg tgcaccaggt gagcctgccc aagcagcccg ccagccagcc ccagggcgac 240
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 cactag 306

<210> 88
 <211> 306

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
tat.cys22.SF162.opt

<400> 88

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aagggcctgg gcatcagcta cggccgcaag aagcgccgcc agcgccgccg cgccccccc 180
gacagcgagg tgcaccaggt gagcctgccc aagcagcccc ccagccagcc ccagggcgac 240
cccaccggcc ccaaggagag caagaagaag gtggagcgcg agaccgagac cgaccccgtg 300
cactag                                           306

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<210> 89

<211> 168

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
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<400> 89

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gcctgcacca actgctactg caagaagtgc tgcttcact gccaggtgtg cttcatcacc 120
aagggcctgg gcatcagcta cggccgcaag aagcgccgcc agcgccgc          168

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<210> 90

<211> 102

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: tat cys22
SF162 protein

<400> 90

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Gln Pro Lys Thr Ala Gly Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
      20              25              30

His Cys Gln Val Cys Phe Ile Thr Lys Gly Leu Gly Ile Ser Tyr Gly
      35              40              45

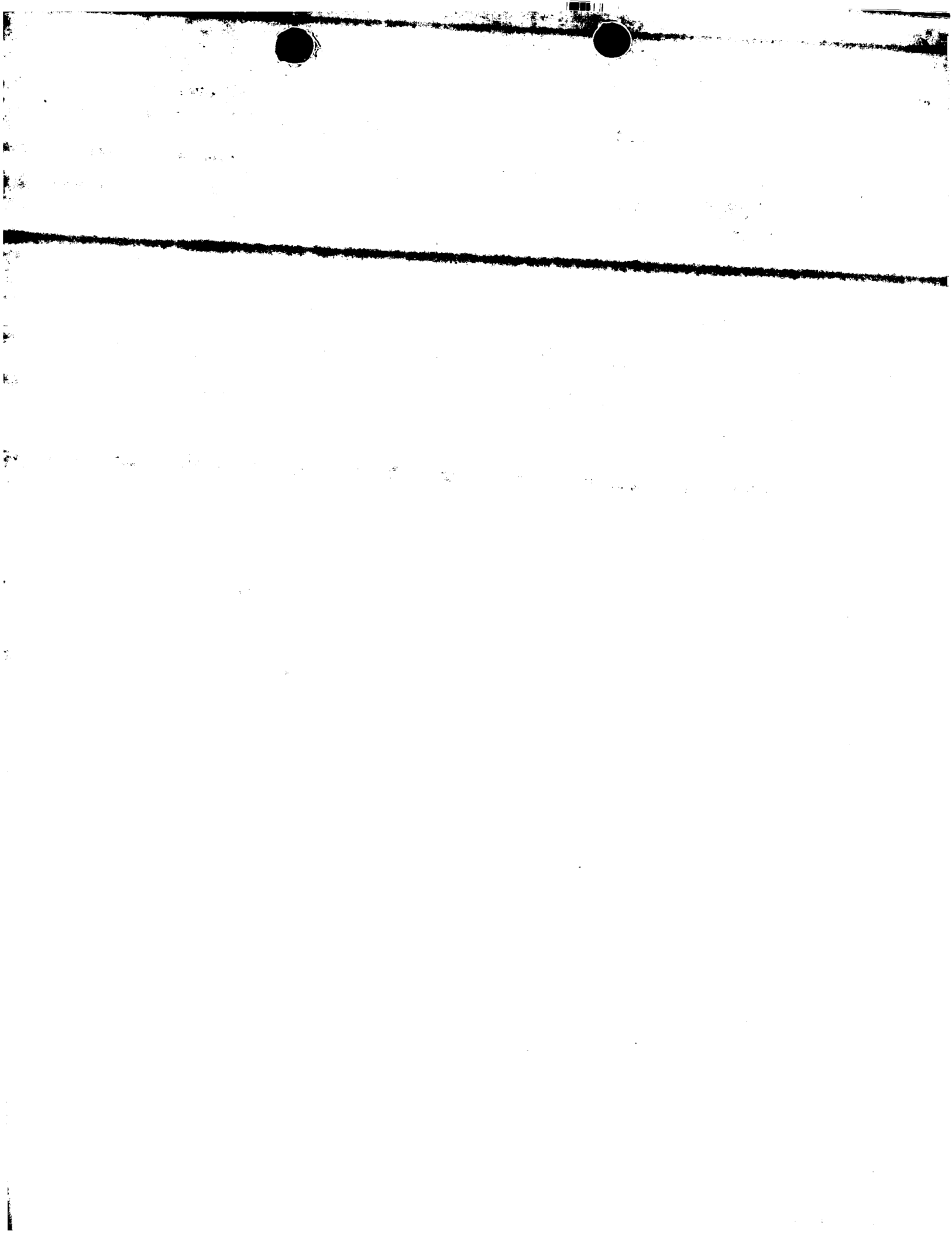
Arg Lys Lys Arg Arg Gln Arg Arg Ala Pro Pro Asp Ser Glu Val
      50              55              60

His Gln Val Ser Leu Pro Lys Gln Pro Ala Ser Gln Pro Gln Gly Asp
      65              70              75              80

Pro Thr Gly Pro Lys Glu Ser Lys Lys Lys Val Glu Arg Glu Thr Glu
      85              90              95

Thr Asp Pro Val His Glx
      100

```



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60/114,495 31 December 1998 (31.12.1998) US
60/168,471 1 December 1999 (01.12.1999) US
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- (72) Inventors: **BARNETT, Susan; Chiron Corporation, 4560 Horton Street - R440, Emeryville, CA 94608 (US). ZUR MEGEDE, Jan; Chiron Corporation, 4560 Horton Street - R440, Emeryville, CA 94608 (US). SRIVASTAVA, Indresh; Chiron Corporation, 4560 Horton Street - R440, Emeryville, CA 94608 (US). LIAN, Ying; Chiron Corporation, 4560 Horton Street - R440, Emeryville, CA 94608 (US). HARTOG, Karin; Chiron Corporation, 4560 Horton Street - R440, Emeryville, CA 94608 (US). LIU, Hong; Chiron Corporation, 4560 Horton Street - R440, Emeryville, CA 94608 (US). GREER, Catherine; Chiron Corporation, 4560 Horton Street - R440, Emeryville, CA 94608 (US). SELBY, Mark; Chiron Corporation,**
- (74) Agents: **DOLLARD, Anne, S.; Chiron Corporation, Intellectual Property - R440, P.O. Box 8097, Emeryville, CA 94662-8097 et al. (US).**
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- Published:
— *With international search report.*
- (88) Date of publication of the international search report:
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- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

(54) Title: **IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION OF VIRUS-LIKE PARTICLES**

(57) Abstract: The present invention relates to the efficient expression of HIV polypeptides in a variety of cell types, including, but not limited to, mammalian, insect, and plant cells. Synthetic expression cassettes encoding the HIV Gag-containing polypeptides are described, as are uses of the expression cassettes in applications including DNA immunization, generation of packaging cell lines, and production of Env-, tat- or Gag-containing proteins. The invention provides methods of producing Virus-Like Particles (VLPs), as well as, uses of the VLPs including, but not limited to, vehicles for the presentation of antigens and stimulation of immune response in subjects to whom the VLPs are administered.

WO 00/39302 A3

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 99/31245

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/49 A61K48/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N A61K C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, STRAND, MEDLINE, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 34640 A (MERCK & CO; SHIVER ET AL.) 13 August 1998 (1998-08-13) cited in the application claims 4,5; examples 3,4 ---	1-4
X	WO 97 31115 A (MERCK & CO; SHIVER ET AL.) 28 August 1997 (1997-08-28) page 54 nucleotides 856-995 example 11 ---	14, 26, 29, 32
X	WO 98 12207 A (GENERAL HOSPITAL CORPORATION) 26 March 1998 (1998-03-26) Figure 1 nucleotides 1315-1458 page 13 -page 21 --- -/--	14, 26, 29, 32

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

* & * document member of the same patent family

Date of the actual completion of the international search

10 August 2000

Date of mailing of the international search report

22.08.00

Name and mailing address of the ISA

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Authorized officer

Cupido, M

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 99/31245

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	WO 99 41397 A (OXFORD BIOMEDICA LTD; KINGSMAN ET AL.) 19 August 1999 (1999-08-19) SEQ ID NO:2 example 2 ---	1-3
E	WO 00 15819 A (CHILDRENS MEDICAL CENTER;GRAY ET AL.) 23 March 2000 (2000-03-23) SEQ ID NO:4,pHDMH ---	1-3
A	SCHNEIDER R ET AL: "Inactivation of the human immunodeficiency virus type 1 inhibitory elements allows rev-independent expression of gag and gag/protease and particle formation" JOURNAL OF VIROLOGY, vol. 71, no. 7, July 1997 (1997-07), pages 4892-4903, XP002137891 AMERICAN SOCIETY FOR MICROBIOLOGY US cited in the application figure 1 ---	1-13, 36-53
A	ANDRE S ET AL: "INCREASED IMMUNE RESPONSE ELICITED BY DNA VACCINATION WITH A SYNTHETIC GP120 SEQUENCE WITH OPTIMIZED CODON USAGE" JOURNAL OF VIROLOGY,US,THE AMERICAN SOCIETY FOR MICROBIOLOGY, vol. 72, no. 2, 1 February 1998 (1998-02-01), pages 1497-1503, XP002073767 ISSN: 0022-538X cited in the application the whole document ---	14,36-53
A	LU S ET AL: "IMMUNOGENICITY OF DNA VACCINES EXPRESSING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENVELOPE GLYCOPROTEIN WITH AND WITHOUT DELETIONS IN THE V1/2 AND V3 REGIONS" AIDS RESEARCH AND HUMAN RETROVIRUSES,US,MARY ANN LIEBERT, vol. 14, no. 2, 20 January 1998 (1998-01-20), pages 151-155, XP000907375 ISSN: 0889-2229 the whole document --- -/--	15,17,20

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 99/31245

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>STAMATATOS L AND CHENG-MAYER C: "An envelope modification that renders a primary, neutralization-resistant clade B HIV-1 isolate highly susceptible to neutralization by sera from other clades" JOURNAL OF VIROLOGY, vol. 72, no. 10, October 1998 (1998-10), pages 7840-7845, XP002139602 AMERICAN SOCIETY FOR MICROBIOLOGY US the whole document</p> <p>-----</p>	15,17,20

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 99/31245

Box I Observation where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Although claims 61-84, 89 and 90 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☒ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-13, 57 and 58 (all completely); 36-56, 60-90 (all partly)

Expression cassette encoding an HIV gag polypeptide, vectors and cells comprising said cassette, uses thereof to produce polypeptides or virus-like particles, methods of treating a subject using said vectors.

2. Claims: 14-35 and 59 (all completely); 36-56 and 60-90 (all partly)

As subject 1 but limited to expression cassettes encoding HIV env polypeptide.

INTERNATIONAL SEARCH REPORT

information on patent family members

International Application No

PCT/US 99/31245

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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WO 0015819 A	23-03-2000	AU 6139699 A	03-04-2000

